SEQUENCE LISTING

<110> Behan, Dominic P.
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Gore, Martin
White, Carol

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agtccattgc ttagatatag ttttgaaacc atggctccca ctggtttgag ttccttgacc 180

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gttgtttgcc tcatggttta ccaaaaagct gccatgaggt ctgcaattaa catcctcctt 360

gccagcctag cttttgcaga catgttgctt gcagtgctga acatgccctt tgccctggta 420

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35 40 45

Glu Thr Met Ala Pro Thr Gly Leu Ser Ser Leu Thr Val Asn Ser Thr
50 55 60

Ala Val Pro Thr Thr Pro Ala Ala Phe Lys Ser Leu Asn Leu Pro Leu
65 70 75 80

Gln Ile Thr Leu Ser Ala Ile Met Ile Phe Ile Leu Phe Val Ser Phe
85 90 95

Leu Gly Asn Leu Val Val Cys Leu Met Val Tyr Gln Lys Ala Ala Met
100 105 110

Arg Ser Ala Ile Asn Ile Leu Leu Ala Ser Leu Ala Phe Ala Asp Met
115 120 125

Leu Leu Ala Val Leu Asn Met Pro Phe Ala Leu Val Thr Ile Leu Thr
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Phe Trp Leu Phe Val Ile Glu Gly Val Ala Ile Leu Leu Ile Ile Ser
                165                 170                 175

Ile Asp Arg Phe Leu Ile Ile Val Gln Arg Gln Asp Lys Leu Asn Pro
            180                 185                 190

Tyr Arg Ala Lys Val Leu Ile Ala Val Ser Trp Ala Thr Ser Phe Cys
        195                 200                 205

Val Ala Phe Pro Leu Ala Val Gly Asn Pro Asp Leu Gln Ile Pro Ser
    210                 215                 220

Arg Ala Pro Gln Cys Val Phe Gly Tyr Thr Thr Asn Pro Gly Tyr Gln
225                 230                 235                 240

Ala Tyr Val Ile Leu Ile Ser Leu Ile Ser Phe Phe Ile Pro Phe Leu
                245                 250                 255

Val Ile Leu Tyr Ser Phe Met Gly Ile Leu Asn Thr Leu Arg His Asn
            260                 265                 270

Ala Leu Arg Ile His Ser Tyr Pro Glu Gly Ile Cys Leu Ser Gln Ala
        275                 280                 285

Ser Lys Leu Gly Leu Met Ser Leu Gln Arg Pro Phe Gln Met Ser Ile
    290                 295                 300

Asp Met Gly Phe Lys Thr Arg Ala Phe Thr Thr Ile Leu Ile Leu Phe
305                 310                 315                 320

Ala Val Phe Ile Val Cys Trp Ala Pro Phe Thr Thr Tyr Ser Leu Val
                325                 330                 335

Ala Thr Phe Ser Lys His Phe Tyr Tyr Gln His Asn Phe Phe Glu Ile
            340                 345                 350

Ser Thr Trp Leu Leu Trp Leu Cys Tyr Leu Lys Ser Ala Leu Asn Pro
        355                 360                 365

Leu Ile Tyr Tyr Trp Arg Ile Lys Lys Phe His Asp Ala Cys Leu Asp
    370                 375                 380

Met Met Pro Lys Ser Phe Lys Phe Leu Pro Gln Leu Pro Gly His Thr
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Lys Arg Arg Ile Arg Pro Ser Ala Val Tyr Val Cys Gly Glu His Arg
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atgtgtaacc tggcggccag cgacctgctc ttcaccctct cgctgcccgt tcgtctctcc 240

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35 40 45

Arg Ala Leu Arg Val His Ser Val Val Ser Val Tyr Met Cys Asn Leu
50 55 60

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Ala Ala Ser Asp Leu Leu Phe Thr Leu Ser Leu Pro Val Arg Leu Ser
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Tyr Tyr Ala Leu His His Trp Pro Phe Pro Asp Leu Leu Cys Gln Thr
                85                  90                  95

Thr Gly Ala Ile Phe Gln Met Asn Met Tyr Gly Ser Cys Ile Phe Leu
            100                 105                 110

Met Leu Ile Asn Val Asp Arg Tyr Ala Ala Ile Val His Pro Leu Arg
        115                 120                 125

Leu Arg His Leu Arg Arg Pro Arg Val Ala Arg Leu Leu Cys Leu Gly
    130                 135                 140

Val Trp Ala Leu Ile Leu Val Phe Ala Val Pro Ala Ala Arg Val His
145                 150                 155                 160

Arg Pro Ser Arg Cys Arg Tyr Arg Asp Leu Glu Val Arg Leu Cys Phe
                165                 170                 175

Glu Ser Phe Ser Asp Glu Leu Trp Lys Gly Arg Leu Leu Pro Leu Val
            180                 185                 190

Leu Leu Ala Glu Ala Leu Gly Phe Leu Leu Pro Leu Ala Ala Val Val
        195                 200                 205

Tyr Ser Ser Gly Arg Val Phe Trp Thr Leu Ala Arg Pro Asp Ala Thr
    210                 215                 220

Gln Ser Gln Arg Arg Arg Lys Thr Val Arg Leu Leu Leu Ala Asn Leu
225                 230                 235                 240

Val Ile Phe Leu Leu Cys Phe Val Pro Tyr Asn Ser Thr Leu Ala Val
                245                 250                 255

Tyr Gly Leu Leu Arg Ser Lys Leu Val Ala Ala Ser Val Pro Ala Arg
            260                 265                 270

Asp Arg Val Arg Gly Val Leu Met Val Met Val Leu Leu Ala Gly Ala
        275                 280                 285

Asn Cys Val Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ala Glu Gly Phe
    290                 295                 300

Arg Asn Thr Leu Arg Gly Leu Gly Thr Pro His Arg Ala Arg Thr Ser
305                 310                 315                 320

Ala Thr Asn Gly Thr Arg Ala Ala Leu Ala Gln Ser Glu Arg Ser Ala
                325                 330                 335

Val Thr Thr Asp Ala Thr Arg Pro Asp Ala Ala Ser Gln Gly Leu Leu
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Asp Ser Ala Leu
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Gly Ala Leu Leu Val Val Val Leu Arg Thr Pro Gly Leu Arg Asp Ala
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Leu Tyr Leu Ala His Leu Cys Val Val Asp Leu Leu Ala Ala Ala Ser
    50                  55                  60

Ile Met Pro Leu Gly Leu Leu Ala Ala Pro Pro Pro Gly Leu Gly Arg
65                  70                  75                  80

Val Arg Leu Gly Pro Ala Pro Cys Arg Ala Ala Arg Phe Leu Ser Ala
                85                  90                  95

Ala Leu Leu Pro Ala Cys Thr Leu Gly Val Ala Ala Leu Gly Leu Ala
            100                 105                 110

Arg Tyr Arg Leu Ile Val His Pro Leu Arg Pro Gly Ser Arg Pro Pro
        115                 120                 125

Pro Val Leu Val Leu Thr Ala Val Trp Ala Ala Ala Gly Leu Leu Gly
    130                 135                 140

Ala Leu Ser Leu Leu Gly Pro Pro Pro Ala Pro Pro Pro Ala Pro Ala
145                 150                 155                 160

Arg Cys Ser Val Leu Ala Gly Gly Leu Gly Pro Phe Arg Pro Leu Trp
                165                 170                 175

Ala Leu Leu Ala Phe Ala Leu Pro Ala Leu Leu Leu Leu Gly Ala Tyr
            180                 185                 190

Gly Gly Ile Phe Val Val Ala Arg Arg Ala Ala Leu Arg Pro Pro Arg
        195                 200                 205

Pro Ala Arg Gly Ser Arg Leu Arg Ser Asp Ser Leu Asp Ser Arg Leu
    210                 215                 220

Ser Ile Leu Pro Pro Leu Arg Pro Arg Leu Pro Gly Gly Lys Ala Ala
225                 230                 235                 240

Leu Ala Pro Ala Leu Ala Val Gly Gln Phe Ala Ala Cys Trp Leu Pro
                245                 250                 255

Tyr Gly Cys Ala Cys Leu Ala Pro Ala Ala Arg Ala Ala Glu Ala Glu
            260                 265                 270

Ala Ala Val Thr Trp Val Ala Tyr Ser Ala Phe Ala Ala His Pro Phe
        275                 280                 285

Leu Tyr Gly Leu Leu Gln Arg Pro Val Arg Leu Ala Leu Gly Arg Leu
    290                 295                 300

Ser Arg Arg Ala Leu Pro Gly Pro Val Arg Ala Cys Thr Pro Gln Ala
305                 310                 315                 320
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Trp His Pro Arg Ala Leu Leu Gln Cys Leu Gln Arg Pro Pro Glu Gly
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Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala
        35                  40                  45

Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp
    50                  55                  60

Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu
65                  70                  75                  80

Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val
                85                  90                  95

Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg
            100                 105                 110

Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly
        115                 120                 125

Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro
    130                 135                 140

Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val
145                 150                 155                 160

Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro
                165                 170                 175

Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala
            180                 185                 190

Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met
        195                 200                 205

Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu
    210                 215                 220

Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro
225                 230                 235                 240

Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu
                245                 250                 255

Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser
            260                 265                 270

Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu
        275                 280                 285

Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe
    290                 295                 300

Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu
305                 310                 315                 320
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        35                  40                  45

Leu Met Ala Trp Leu Ala Gly Ser Gln Ala Arg His Gly Ala Gly Thr
    50                  55                  60

Arg Leu Ala Leu Leu Leu Leu Leu Ser Leu Ala Leu Ser Asp Phe Leu Phe
65                  70                  75                  80

Leu Ala Ala Ala Ala Phe Gln Ile Leu Glu Ile Arg His Gly Gly His
                85                  90                  95

Trp Pro Leu Gly Thr Ala Ala Cys Arg Phe Tyr Tyr Phe Leu Trp Gly
            100                 105                 110

Val Ser Tyr Ser Ser Gly Leu Phe Leu Leu Ala Ala Leu Ser Leu Asp
        115                 120                 125

Arg Cys Leu Leu Ala Leu Cys Pro His Trp Tyr Pro Gly His Arg Pro
    130                 135                 140

Val Arg Leu Pro Leu Trp Val Cys Ala Gly Val Trp Val Leu Ala Thr
145                 150                 155                 160

Leu Phe Ser Val Pro Trp Leu Val Phe Pro Glu Ala Ala Val Trp Trp
                165                 170                 175

Tyr Asp Leu Val Ile Cys Leu Asp Phe Trp Asp Ser Glu Glu Leu Ser
            180                 185                 190

Leu Arg Met Leu Glu Val Leu Gly Gly Phe Leu Pro Phe Leu Leu Leu
        195                 200                 205

Leu Val Cys His Val Leu Thr Gln Ala Thr Arg Thr Cys His Arg Gln
    210                 215                 220

Gln Gln Pro Ala Ala Cys Arg Gly Phe Ala Arg Val Ala Arg Thr Ile
225                 230                 235                 240

Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr Gln Leu Ala Gln Leu
                245                 250                 255

Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser Gly Tyr Leu Leu Trp
            260                 265                 270

Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu Leu Asn Ser Cys Leu
        275                 280                 285
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Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp Leu Arg Thr Leu Leu
290 295 300

Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu Cys Glu Glu Arg Pro
305 310 315 320

Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln Leu Asp Ser Glu Gly
325 330 335

Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln Ser Gln Met Asp Pro
340 345 350

Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln Pro Arg Ser Asp Pro
355 360 365

Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln Pro Gln Ser Asp Pro
370 375 380

Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln Pro Gln Ser Asp Ser
385 390 395 400

Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln Thr Pro Ala Pro Ala
405 410 415

Ala Ser Ser Val Pro Ser Pro Cys Asp Glu Ala Ser Pro Thr Pro Ser
420 425 430

Ser His Pro Thr Pro Gly Ala Leu Glu Asp Pro Ala Thr Pro Pro Ala
435 440 445

Ser Glu Gly Glu Ser Pro Ser Ser Thr Pro Pro Glu Ala Ala Pro Gly
450 455 460

Ala Gly Pro Thr
465

<210> 11
<211> 1248
<212> DNA
<213> Homo sapiens

<400> 11
atgtcaggga tggaaaaact tcagaatgct tcctggatct accagcagaa actagaagat 60

ccattccaga aacacctgaa cagcaccgag gagtatctgg ccttcctctg cggacctcgg 120

cgcagccact tcttcctccc cgtgtctgtg gtgtatgtgc caatttttgt ggtgggggtc 180

attggcaatg tcctggtgtg cctggtgatt ctgcagcacc aggctatgaa gacgcccacc 240

aactactacc tcttcagcct ggcggtctct gacctcctgg tcctgctcct tggaatgccc 300

ctggaggtct atgagatgtg gcgcaactac cctttcttgt tcgggcccgt gggctgctac 360

ttcaagacgg ccctctttga gaccgtgtgc ttcgcctcca tcctcagcat caccaccgtc 420

agcgtggagc gctacgtggc catcctacac ccgttccgcg ccaaactgca gagcacccgg 480

cgccgggccc tcaggatcct cggcatcgtc tggggcttct ccgtgctctt ctccctgccc 540

aacaccagca tccatggcat caagttccac tacttcccca atgggtccct ggtcccaggt 600

tcggccacct gtacggtcat caagcccatg tggatctaca atttcatcat ccaggtcacc 660

tccttcctat tctacctcct ccccatgact gtcatcagtg tcctctacta cctcatggca 720

ctcagactaa agaaagacaa atctcttgag gcagatgaag ggaatgcaaa tattcaaaga 780

ccctgcagaa aatcagtcaa caagatgctg tttgtcttgg tcttagtgtt tgctatctgt 840

tgggccccgt tccacattga ccgactcttc ttcagctttg tggaggagtg gagtgaatcc 900

ctggctgctg tgttcaacct cgtccatgtg gtgtcaggtg tcttcttcta cctgagctca 960

gctgtcaacc ccattatcta taacctactg tctcgccgct tccaggcagc attccagaat 1020

gtgatctctt ctttccacaa acagtggcac tcccagcatg acccacagtt gccacctgcc 1080

cagcggaaca tcttcctgac agaatgccac tttgtggagc tgaccgaaga tataggtccc 1140

caattcccat gtcagtcatc catgcacaac tctcacctcc caacagccct ctctagtgaa 1200

cagatgtcaa gaacaaacta tcaaagcttc cactttaaca aaacctga 1248

<210> 12
<211> 415
<212> PRT
<213> Homo sapiens

<400> 12

Met Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln
1 5 10 15

Lys Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr
20 25 30

Leu Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val
35 40 45

Ser Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val
50 55 60

Leu Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr
65 70 75 80

Asn Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu
85 90 95

Leu Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe
100 105 110

Leu Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr
115 120 125

Val Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg
130 135 140

```
Tyr Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg
145                 150                 155                 160

Arg Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu
                165                 170                 175

Phe Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe
            180                 185                 190

Pro Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys
        195                 200                 205

Pro Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe
    210                 215                 220

Tyr Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala
225                 230                 235                 240

Leu Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala
                245                 250                 255

Asn Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val
            260                 265                 270

Leu Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg
        275                 280                 285

Leu Phe Phe Ser Phe Val Glu Glu Trp Ser Glu Ser Leu Ala Ala Val
    290                 295                 300

Phe Asn Leu Val His Val Val Ser Gly Val Phe Phe Tyr Leu Ser Ser
305                 310                 315                 320

Ala Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala
                325                 330                 335

Ala Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln
            340                 345                 350

His Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu
        355                 360                 365

Cys His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys
    370                 375                 380

Gln Ser Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu
385                 390                 395                 400

Gln Met Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr
                405                 410                 415
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<210> 13
<211> 1173

<212> DNA
<213> Homo sapiens

<400> 13
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tttatgtcct tagtagcttt tgctataatg ctaggaaatg ctttggtcat tttagctttt 120

gtggtggaca aaaaccttag acatcgaagt agttattttt ttcttaactt ggccatctct 180

gacttctttg tgggtgtgat ctccattcct ttgtacatcc ctcacacgct gttcgaatgg 240

gattttggaa aggaaatctg tgtattttgg ctcactactg actatctgtt atgtacagca 300

tctgtatata acattgtcct catcagctat gatcgatacc tgtcagtctc aaatgctgtg 360

tcttatagaa ctcaacatac tggggtcttg aagattgtta ctctgatggt ggccgtttgg 420

gtgctggcct tcttagtgaa tgggccaatg attctagttt cagagtcttg gaaggatgaa 480

ggtagtgaat gtgaacctgg attttttttcg gaatggtaca tccttgccat cacatcattc 540

ttggaattcg tgatcccagt catcttagtc gcttatttca acatgaatat ttattggagc 600

ctgtggaagc gtgatcatct cagtaggtgc caaagccatc ctggactgac tgctgtctct 660

tccaacatct gtggacactc attcagaggt agactatctt caaggagatc tctttctgca 720

tcgacagaag ttcctgcatc ctttcattca gagagacaga ggagaaagag tagtctcatg 780

ttttcctcaa gaaccaagat gaatagcaat acaattgctt ccaaaatggg ttccttctcc 840

caatcagatt ctgtagctct tcaccaaagg gaacatgttg aactgcttag agccaggaga 900

ttagccaagt cactggccat tctcttaggg gtttttgctg tttgctgggc tccatattct 960

ctgttcacaa ttgtcctttc attttattcc tcagcaacag gtcctaaatc agtttggtat 1020

agaattgcat tttggcttca gtggttcaat tcctttgtca atcctctttt gtatccattg 1080

tgtcacaagc gctttcaaaa ggctttcttg aaaatatttt gtataaaaaa gcaacctcta 1140

ccatcacaac acagtcggtc agtatcttct taa 1173

<210> 14
<211> 390
<212> PRT
<213> Homo sapiens

<400> 14

Met Pro Asp Thr Asn Ser Thr Ile Asn Leu Ser Leu Ser Thr Arg Val
1 5 10 15

Thr Leu Ala Phe Phe Met Ser Leu Val Ala Phe Ala Ile Met Leu Gly
20 25 30

Asn Ala Leu Val Ile Leu Ala Phe Val Val Asp Lys Asn Leu Arg His
35 40 45

Arg Ser Ser Tyr Phe Phe Leu Asn Leu Ala Ile Ser Asp Phe Phe Val
50 55 60

Gly Val Ile Ser Ile Pro Leu Tyr Ile Pro His Thr Leu Phe Glu Trp
65 70 75 80

```
Asp Phe Gly Lys Glu Ile Cys Val Phe Trp Leu Thr Thr Asp Tyr Leu
                85                  90                  95

Leu Cys Thr Ala Ser Val Tyr Asn Ile Val Leu Ile Ser Tyr Asp Arg
            100                 105                 110

Tyr Leu Ser Val Ser Asn Ala Val Ser Tyr Arg Thr Gln His Thr Gly
        115                 120                 125

Val Leu Lys Ile Val Thr Leu Met Val Ala Val Trp Val Leu Ala Phe
    130                 135                 140

Leu Val Asn Gly Pro Met Ile Leu Val Ser Glu Ser Trp Lys Asp Glu
145                 150                 155                 160

Gly Ser Glu Cys Glu Pro Gly Phe Phe Ser Glu Trp Tyr Ile Leu Ala
                165                 170                 175

Ile Thr Ser Phe Leu Glu Phe Val Ile Pro Val Ile Leu Val Ala Tyr
            180                 185                 190

Phe Asn Met Asn Ile Tyr Trp Ser Leu Trp Lys Arg Asp His Leu Ser
        195                 200                 205

Arg Cys Gln Ser His Pro Gly Leu Thr Ala Val Ser Ser Asn Ile Cys
    210                 215                 220

Gly His Ser Phe Arg Gly Arg Leu Ser Ser Arg Arg Ser Leu Ser Ala
225                 230                 235                 240

Ser Thr Glu Val Pro Ala Ser Phe His Ser Glu Arg Gln Arg Arg Lys
                245                 250                 255

Ser Ser Leu Met Phe Ser Ser Arg Thr Lys Met Asn Ser Asn Thr Ile
            260                 265                 270

Ala Ser Lys Met Gly Ser Phe Ser Gln Ser Asp Ser Val Ala Leu His
        275                 280                 285

Gln Arg Glu His Val Glu Leu Leu Arg Ala Arg Arg Leu Ala Lys Ser
    290                 295                 300

Leu Ala Ile Leu Leu Gly Val Phe Ala Val Cys Trp Ala Pro Tyr Ser
305                 310                 315                 320

Leu Phe Thr Ile Val Leu Ser Phe Tyr Ser Ser Ala Thr Gly Pro Lys
                325                 330                 335

Ser Val Trp Tyr Arg Ile Ala Phe Trp Leu Gln Trp Phe Asn Ser Phe
            340                 345                 350
```

Val Asn Pro Leu Leu Tyr Pro Leu Cys His Lys Arg Phe Gln Lys Ala
355 360 365

Phe Leu Lys Ile Phe Cys Ile Lys Lys Gln Pro Leu Pro Ser Gln His
370 375 380

Ser Arg Ser Val Ser Ser
385 390

<210> 15
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 15
ggaaagctta acgatcccca ggagcaacat 30

<210> 16
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 16
ctgggatcct acgagagcat ttttcacaca g 31

<210> 17
<211> 1128
<212> DNA
<213> Homo sapiens

<400> 17
atggcgaacg cgagcgagcc gggtggcagc ggcggcggcg aggcggccgc cctgggcctc 60

aagctggcca cgctcagcct gctgctgtgc gtgagcctag cgggcaacgt gctgttcgcg 120

ctgctgatcg tgcgggagcg cagcctgcac cgcgccccgt actacctgct gctcgacctg 180

tgcctggccg acgggctgcg cgcgctcgcc tgcctcccgg ccgtcatgct ggcggcgcgg 240

cgtgcggcgg ccgcggcggg ggcgccgccg ggcgcgctgg gctgcaagct gctcgccttc 300

ctggccgcgc tcttctgctt ccacgccgcc ttcctgctgc tgggcgtggg cgtcacccgc 360

tacctggcca tcgcgcacca ccgcttctat gcagagcgcc tggccggctg gccgtgcgcc 420

gccatgctgg tgtgcgccgc ctgggcgctg gcgctggccg cggccttccc gccagtgctg 480

gacggcggtg gcgacgacga ggacgcgccg tgcgccctgg agcagcggcc cgacggcgcc 540

cccggcgcgc tgggcttcct gctgctgctg gccgtggtgg tgggcgccac gcacctcgtc 600

tacctccgcc tgctcttctt catccacgac cgccgcaaga tgcggcccgc gcgcctggtg 660

cccgccgtca gccacgactg gaccttccac ggcccgggcg ccaccggcca ggcggccgcc 720

aactggacgg cgggcttcgg ccgcgggccc acgccgcccg cgcttgtggg catccggccc 780

gcagggccgg gccgcggcgc gcgccgcctc ctcgtgctgg aagaattcaa gacggagaag 840

aggctgtgca agatgttcta cgccgtcacg ctgctcttcc tgctcctctg ggggccctac 900

gtcgtggcca gctacctgcg ggtcctggtg cggcccggcg ccgtccccca ggcctacctg 960

acggcctccg tgtggctgac cttcgcgcag gccggcatca accccgtcgt gtgcttcctc 1020

ttcaacaggg agctgaggga ctgcttcagg gcccagttcc cctgctgcca gagcccccgg 1080

accacccagg cgacccatcc ctgcgacctg aaaggcattg gtttatga 1128

<210> 18
<211> 375
<212> PRT
<213> Homo sapiens

<400> 18

Met Ala Asn Ala Ser Glu Pro Gly Gly Ser Gly Gly Gly Glu Ala Ala
1 5 10 15

Ala Leu Gly Leu Lys Leu Ala Thr Leu Ser Leu Leu Leu Cys Val Ser
20 25 30

Leu Ala Gly Asn Val Leu Phe Ala Leu Leu Ile Val Arg Glu Arg Ser
35 40 45

Leu His Arg Ala Pro Tyr Tyr Leu Leu Leu Asp Leu Cys Leu Ala Asp
50 55 60

Gly Leu Arg Ala Leu Ala Cys Leu Pro Ala Val Met Leu Ala Ala Arg
65 70 75 80

Arg Ala Ala Ala Ala Ala Gly Ala Pro Pro Gly Ala Leu Gly Cys Lys
85 90 95

Leu Leu Ala Phe Leu Ala Ala Leu Phe Cys Phe His Ala Ala Phe Leu
100 105 110

Leu Leu Gly Val Gly Val Thr Arg Tyr Leu Ala Ile Ala His His Arg
115 120 125

Phe Tyr Ala Glu Arg Leu Ala Gly Trp Pro Cys Ala Ala Met Leu Val
130 135 140

Cys Ala Ala Trp Ala Leu Ala Leu Ala Ala Ala Phe Pro Pro Val Leu
145 150 155 160

Asp Gly Gly Gly Asp Asp Glu Asp Ala Pro Cys Ala Leu Glu Gln Arg
165 170 175

Pro Asp Gly Ala Pro Gly Ala Leu Gly Phe Leu Leu Leu Leu Ala Val
180 185 190

Val Val Gly Ala Thr His Leu Val Tyr Leu Arg Leu Leu Phe Phe Ile
195 200 205

```
His Asp Arg Arg Lys Met Arg Pro Ala Arg Leu Val Pro Ala Val Ser
    210                 215                 220

His Asp Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln Ala Ala Ala
225                 230                 235                 240

Asn Trp Thr Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Ala Leu Val
                245                 250                 255

Gly Ile Arg Pro Ala Gly Pro Gly Arg Gly Ala Arg Arg Leu Leu Val
            260                 265                 270

Leu Glu Glu Phe Lys Thr Glu Lys Arg Leu Cys Lys Met Phe Tyr Ala
        275                 280                 285

Val Thr Leu Leu Phe Leu Leu Leu Trp Gly Pro Tyr Val Val Ala Ser
    290                 295                 300

Tyr Leu Arg Val Leu Val Arg Pro Gly Ala Val Pro Gln Ala Tyr Leu
305                 310                 315                 320

Thr Ala Ser Val Trp Leu Thr Phe Ala Gln Ala Gly Ile Asn Pro Val
                325                 330                 335

Val Cys Phe Leu Phe Asn Arg Glu Leu Arg Asp Cys Phe Arg Ala Gln
            340                 345                 350

Phe Pro Cys Cys Gln Ser Pro Arg Thr Thr Gln Ala Thr His Pro Cys
        355                 360                 365

Asp Leu Lys Gly Ile Gly Leu
    370                 375
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<210> 19
<211> 1002
<212> DNA
<213> Homo sapiens

<400> 19

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atgaacacca cagtgatgca aggcttcaac agatctgagc ggtgccccag agacactcgg     60

atagtacagc tggtattccc agccctctac acagtggttt tcttgaccgg catcctgctg    120

aatactttgg ctctgtgggt gtttgttcac atccccagct cctccacctt catcatctac    180

ctcaaaaaca ctttggtggc cgacttgata atgacactca tgcttccttt caaaatcctc    240

tctgactcac acctggcacc ctggcagctc agagcttttg tgtgtcgttt ttcttcggtg    300

atattttatg agaccatgta tgtgggcatc gtgctgttag ggctcatagc ctttgacaga    360

ttcctcaaga tcatcagacc tttgagaaat atttttctaa aaaaacctgt ttttgcaaaa    420

acggtctcaa tcttcatctg gttcttttg ttcttcatct ccctgccaaa tacgatcttg     480

agcaacaagg aagcaacacc atcgtctgtg aaaaagtgtg cttccttaaa ggggcctctg    540

gggctgaaat ggcatcaaat ggtaaataac atatgccagt ttatttttctg gactgttttt    600
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atcctaatgc ttgtgtttta tgtggttatt gcaaaaaaag tatatgattc ttatagaaag 660

tccaaaagta aggacagaaa aaacaacaaa aagctggaag gcaaagtatt tgttgtcgtg 720

gctgtcttct ttgtgtgttt tgctccattt cattttgcca gagttccata tactcacagt 780

caaaccaaca ataagactga ctgtagactg caaaatcaac tgtttattgc taaagaaaca 840

actctctttt tggcagcaac taacatttgt atggatccct taatatacat attcttatgt 900

aaaaaattca cagaaaagct accatgtatg caagggagaa agaccacagc atcaagccaa 960

gaaaatcata gcagtcagac agacaacata accttaggct ga 1002

<210> 20
<211> 333
<212> PRT
<213> Homo sapiens

<400> 20

Met Asn Thr Thr Val Met Gln Gly Phe Asn Arg Ser Glu Arg Cys Pro
1 5 10 15

Arg Asp Thr Arg Ile Val Gln Leu Val Phe Pro Ala Leu Tyr Thr Val
20 25 30

Val Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu Ala Leu Trp Val Phe
35 40 45

Val His Ile Pro Ser Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr
50 55 60

Leu Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile Leu
65 70 75 80

Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys Arg
85 90 95

Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val Leu
100 105 110

Leu Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro Leu
115 120 125

Arg Asn Ile Phe Leu Lys Lys Pro Val Phe Ala Lys Thr Val Ser Ile
130 135 140

Phe Ile Trp Phe Phe Leu Phe Phe Ile Ser Leu Pro Asn Thr Ile Leu
145 150 155 160

Ser Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser Leu
165 170 175

Lys Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile Cys
180 185 190

```
Gln Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr Val
        195                 200                 205

Val Ile Ala Lys Lys Val Tyr Asp Ser Tyr Arg Lys Ser Lys Ser Lys
    210                 215                 220

Asp Arg Lys Asn Asn Lys Lys Leu Glu Gly Lys Val Phe Val Val Val
225                 230                 235                 240

Ala Val Phe Phe Val Cys Phe Ala Pro Phe His Phe Ala Arg Val Pro
                245                 250                 255

Tyr Thr His Ser Gln Thr Asn Asn Lys Thr Asp Cys Arg Leu Gln Asn
            260                 265                 270

Gln Leu Phe Ile Ala Lys Glu Thr Thr Leu Phe Leu Ala Ala Thr Asn
        275                 280                 285

Ile Cys Met Asp Pro Leu Ile Tyr Ile Phe Leu Cys Lys Lys Phe Thr
    290                 295                 300

Glu Lys Leu Pro Cys Met Gln Gly Arg Lys Thr Thr Ala Ser Ser Gln
305                 310                 315                 320

Glu Asn His Ser Ser Gln Thr Asp Asn Ile Thr Leu Gly
                325                 330
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<210> 21
<211> 1122
<212> DNA
<213> Homo sapiens

<400> 21

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atggccaaca ctaccggaga gcctgaggag gtgagcggcg ctctgtcccc accgtccgca     60

tcagcttatg tgaagctggt actgctggga ctgattatgt gcgtgagcct ggcgggtaac    120

gccatcttgt ccctgctggt gctcaaggag cgtgccctgc acaaggctcc ttactacttc    180

ctgctggacc tgtgcctggc cgatggcata cgctctgccg tctgcttccc ctttgtgctg    240

gcttctgtgc gccacggctc ttcatggacc ttcagtgcac tcagctgcaa gattgtggcc    300

tttatggccg tgctcttttg cttccatgcg gccttcatgc tgttctgcat cagcgtcacc    360

cgctacatgg ccatcgccca ccaccgcttc tacgccaagc gcatgacact ctggacatgc    420

gcggctgtca tctgcatggc ctggaccctg tctgtggcca tggccttccc acctgtcttt    480

gacgtgggca cctacaagtt tattcgggag gaggaccagt gcatctttga gcatcgctac    540

ttcaaggcca atgacacgct gggcttcatg cttatgttgg ctgtgctcat ggcagctacc    600

catgctgtct acggcaagct gctcctcttc gagtatcgtc accgcaagat gaagccagtg    660

cagatggtgc cagccatcag ccagaactgg acattccatg gtcccggggc caccggccag    720

gctgctgcca actggatcgc cggctttggc cgtgggccca tgccaccaac cctgctgggt    780

atccggcaga atgggcatgc agccagccgg cggctactgg gcatggacga ggtcaagggt    840
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gaaaagcagc tgggccgcat gttctacgcg atcacactgc tctttctgct cctctggtca 900

ccctacatcg tggcctgcta ctggcgagtg tttgtgaaag cctgtgctgt gccccaccgc 960

tacctggcca ctgctgtttg gatgagcttc gcccaggctg ccgtcaaccc aattgtctgc 1020

ttcctgctca acaaggacct caagaagtgc ctgaccactc acgccccctg ctggggcaca 1080

ggaggtgccc cggctcccag agaaccctac tgtgtcatgt ga 1122

<210> 22
<211> 373
<212> PRT
<213> Homo sapiens

<400> 22

Met Ala Asn Thr Thr Gly Glu Pro Glu Glu Val Ser Gly Ala Leu Ser
1 5 10 15

Pro Pro Ser Ala Ser Ala Tyr Val Lys Leu Val Leu Leu Gly Leu Ile
20 25 30

Met Cys Val Ser Leu Ala Gly Asn Ala Ile Leu Ser Leu Leu Val Leu
35 40 45

Lys Glu Arg Ala Leu His Lys Ala Pro Tyr Tyr Phe Leu Leu Asp Leu
50 55 60

Cys Leu Ala Asp Gly Ile Arg Ser Ala Val Cys Phe Pro Phe Val Leu
65 70 75 80

Ala Ser Val Arg His Gly Ser Ser Trp Thr Phe Ser Ala Leu Ser Cys
85 90 95

Lys Ile Val Ala Phe Met Ala Val Leu Phe Cys Phe His Ala Ala Phe
100 105 110

Met Leu Phe Cys Ile Ser Val Thr Arg Tyr Met Ala Ile Ala His His
115 120 125

Arg Phe Tyr Ala Lys Arg Met Thr Leu Trp Thr Cys Ala Ala Val Ile
130 135 140

Cys Met Ala Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Phe
145 150 155 160

Asp Val Gly Thr Tyr Lys Phe Ile Arg Glu Glu Asp Gln Cys Ile Phe
165 170 175

Glu His Arg Tyr Phe Lys Ala Asn Asp Thr Leu Gly Phe Met Leu Met
180 185 190

Leu Ala Val Leu Met Ala Ala Thr His Ala Val Tyr Gly Lys Leu Leu
195 200 205

Leu Phe Glu Tyr Arg His Arg Lys Met Lys Pro Val Gln Met Val Pro
210 215 220

Ala Ile Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln
225 230 235 240

Ala Ala Ala Asn Trp Ile Ala Gly Phe Gly Arg Gly Pro Met Pro Pro
245 250 255

Thr Leu Leu Gly Ile Arg Gln Asn Gly His Ala Ala Ser Arg Arg Leu
260 265 270

Leu Gly Met Asp Glu Val Lys Gly Glu Lys Gln Leu Gly Arg Met Phe
275 280 285

Tyr Ala Ile Thr Leu Leu Phe Leu Leu Leu Trp Ser Pro Tyr Ile Val
290 295 300

Ala Cys Tyr Trp Arg Val Phe Val Lys Ala Cys Ala Val Pro His Arg
305 310 315 320

Tyr Leu Ala Thr Ala Val Trp Met Ser Phe Ala Gln Ala Ala Val Asn
325 330 335

Pro Ile Val Cys Phe Leu Leu Asn Lys Asp Leu Lys Lys Cys Leu Thr
340 345 350

Thr His Ala Pro Cys Trp Gly Thr Gly Gly Ala Pro Ala Pro Arg Glu
355 360 365

Pro Tyr Cys Val Met
370

<210> 23
<211> 1053
<212> DNA
<213> Homo sapiens

<400> 23
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acttatgact acagtcaata tgaattgatc tgtatcaaag aagatgtcag agaatttgca 120

aaagttttcc tccctgtatt cctcacaata gctttcgtca ttggacttgc aggcaattcc 180

atggtagtgg caatttatgc ctattacaag aaacagagaa ccaaaacaga tgtgtacatc 240

ctgaatttgg ctgtagcaga tttactcctt ctattcactc tgccttttg ggctgttaat 300

gcagttcatg ggtgggtttt agggaaaata atgtgcaaaa taacttcagc cttgtacaca 360

ctaaactttg tctctggaat gcagtttctg gcttgcatca gcatagacag atatgtggca 420

gtaactaatg tccccagcca atcaggagtg ggaaaaccat gctggatcat ctgtttctgt 480

gtctggatgg ctgccatctt gctgagcata ccccagctgg ttttttatac agtaaatgac 540

aatgctaggt gcattcccat tttcccccgc tacctaggaa catcaatgaa agcattgatt 600

caaatgctag agatctgcat tggatttgta gtacccttc ttattatggg ggtgtgctac 660

tttatcacgg caaggacact catgaagatg ccaaacatta aaatatctcg acccctaaaa 720

gttctgctca cagtcgttat agttttcatt gtcactcaac tgccttataa cattgtcaag 780

ttctgccgag ccatagacat catctactcc ctgatcacca gctgcaacat gagcaaacgc 840

atggacatcg ccatccaagt cacagaaagc attgcactct ttcacagctg cctcaaccca 900

atcctttatg tttttatggg agcatctttc aaaaactacg ttatgaaagt ggccaagaaa 960

tatgggtcct ggagaagaca gagacaaagt gtggaggagt ttccttttga ttctgagggt 1020

cctacagagc caaccagtac ttttagcatt taa 1053

<210> 24
<211> 350
<212> PRT
<213> Homo sapiens

<400> 24

Met Ala Leu Glu Gln Asn Gln Ser Thr Asp Tyr Tyr Tyr Glu Glu Asn
1 5 10 15

Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile
20 25 30

Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu
35 40 45

Thr Ile Ala Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala
50 55 60

Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile
65 70 75 80

Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Leu Phe Thr Leu Pro Phe
85 90 95

Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys
100 105 110

Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln
115 120 125

Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Asn Val
130 135 140

Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys
145 150 155 160

Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr
165 170 175

Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu
180 185 190

```
Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly
        195                 200                 205

Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala
    210                 215                 220

Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys
225                 230                 235                 240

Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr
                245                 250                 255

Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile
            260                 265                 270

Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr
        275                 280                 285

Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val
    290                 295                 300

Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys
305                 310                 315                 320

Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe
                325                 330                 335

Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile
            340                 345                 350
```

<210> 25
<211> 1116
<212> DNA
<213> Homo sapiens

<400> 25
atgccaggaa acgccacccc agtgaccacc actgccccgt gggcctccct gggcctctcc 60

gccaagacct gcaacaacgt gtccttcgaa gagagcagga tagtcctggt cgtggtgtac 120

agcgcggtgt gcacgctggg ggtgccggcc aactgcctga ctgcgtggct ggcgctgctg 180

caggtactgc agggcaacgt gctggccgtc tacctgctct gcctggcact ctgcgaactg 240

ctgtacacag gcacgctgcc actctgggtc atctatatcc gcaaccagca ccgctggacc 300

ctaggcctgc tggcctcgaa ggtgaccgcc tacatcttct tctgcaacat ctacgtcagc 360

atcctcttcc tgtgctgcat ctcctgcgac cgcttcgtgg ccgtggtgta cgcgctggag 420

agtcggggcc gccgccgccg gaggaccgcc atcctcatct ccgcctgcat cttcatcctc 480

gtcgggatcg ttcactaccc ggtgttccag acggaagaca aggagacctg ctttgacatg 540

ctgcagatgg acagcaggat tgccgggtac tactacgcca ggttcaccgt tggctttgcc 600

atccctctct ccatcatcgc cttcaccaac caccggattt tcaggagcat caagcagagc 660

atgggcttaa gcgctgccca gaaggccaag gtgaagcact cggccatcgc ggtggttgtc 720

atcttcctag tctgcttcgc cccgtaccac ctggttctcc tcgtcaaagc cgctgccttt 780

tcctactaca gaggagacag gaacgccatg tgcggcttgg aggaaaggct gtacacagcc 840

tctgtggtgt ttctgtgcct gtccacggtg aacggcgtgg ctgaccccat tatctacgtg 900

ctggccacgg accattcccg ccaagaagtg tccagaatcc ataaggggtg gaaagagtgg 960

tccatgaaga cagacgtcac caggctcacc cacagcaggg acaccgagga gctgcagtcg 1020

cccgtggccc ttgcagacca ctacaccttc tccaggcccg tgcacccacc agggtcacca 1080

tgccctgcaa agaggctgat tgaggagtcc tgctga 1116

<210> 26
<211> 371
<212> PRT
<213> Homo sapiens

<400> 26

Met Pro Gly Asn Ala Thr Pro Val Thr Thr Thr Ala Pro Trp Ala Ser
1 5 10 15

Leu Gly Leu Ser Ala Lys Thr Cys Asn Asn Val Ser Phe Glu Glu Ser
20 25 30

Arg Ile Val Leu Val Val Val Tyr Ser Ala Val Cys Thr Leu Gly Val
35 40 45

Pro Ala Asn Cys Leu Thr Ala Trp Leu Ala Leu Leu Gln Val Leu Gln
50 55 60

Gly Asn Val Leu Ala Val Tyr Leu Leu Cys Leu Ala Leu Cys Glu Leu
65 70 75 80

Leu Tyr Thr Gly Thr Leu Pro Leu Trp Val Ile Tyr Ile Arg Asn Gln
85 90 95

His Arg Trp Thr Leu Gly Leu Leu Ala Ser Lys Val Thr Ala Tyr Ile
100 105 110

Phe Phe Cys Asn Ile Tyr Val Ser Ile Leu Phe Leu Cys Cys Ile Ser
115 120 125

Cys Asp Arg Phe Val Ala Val Val Tyr Ala Leu Glu Ser Arg Gly Arg
130 135 140

Arg Arg Arg Arg Thr Ala Ile Leu Ile Ser Ala Cys Ile Phe Ile Leu
145 150 155 160

Val Gly Ile Val His Tyr Pro Val Phe Gln Thr Glu Asp Lys Glu Thr
165 170 175

Cys Phe Asp Met Leu Gln Met Asp Ser Arg Ile Ala Gly Tyr Tyr Tyr
180 185 190

```
Ala Arg Phe Thr Val Gly Phe Ala Ile Pro Leu Ser Ile Ile Ala Phe
        195                 200                 205

Thr Asn His Arg Ile Phe Arg Ser Ile Lys Gln Ser Met Gly Leu Ser
    210                 215                 220

Ala Ala Gln Lys Ala Lys Val Lys His Ser Ala Ile Ala Val Val Val
225                 230                 235                 240

Ile Phe Leu Val Cys Phe Ala Pro Tyr His Leu Val Leu Leu Val Lys
                245                 250                 255

Ala Ala Ala Phe Ser Tyr Tyr Arg Gly Asp Arg Asn Ala Met Cys Gly
            260                 265                 270

Leu Glu Glu Arg Leu Tyr Thr Ala Ser Val Val Phe Leu Cys Leu Ser
        275                 280                 285

Thr Val Asn Gly Val Ala Asp Pro Ile Ile Tyr Val Leu Ala Thr Asp
    290                 295                 300

His Ser Arg Gln Glu Val Ser Arg Ile His Lys Gly Trp Lys Glu Trp
305                 310                 315                 320

Ser Met Lys Thr Asp Val Thr Arg Leu Thr His Ser Arg Asp Thr Glu
                325                 330                 335

Glu Leu Gln Ser Pro Val Ala Leu Ala Asp His Tyr Thr Phe Ser Arg
            340                 345                 350

Pro Val His Pro Pro Gly Ser Pro Cys Pro Ala Lys Arg Leu Ile Glu
        355                 360                 365

Glu Ser Cys
    370
```

<210> 27
<211> 1113
<212> DNA
<213> Homo sapiens

<400> 27
atggcgaact atagccatgc agctgacaac attttgcaaa atctctcgcc tctaacagcc 60

tttctgaaac tgacttcctt gggtttcata ataggagtca gcgtggtggg caacctcctg 120

atctccattt tgctagtgaa agataagacc ttgcatagag caccttacta cttcctgttg 180

gatctttgct gttcagatat cctcagatct gcaatttgtt tcccatttgt gttcaactct 240

gtcaaaaatg gctctacctg gacttatggg actctgactt gcaaagtgat tgcctttctg 300

ggggttttgt cctgtttcca cactgctttc atgctcttct gcatcagtgt caccagatac 360

ttagctatcg cccatcaccg cttctataca aagaggctga ccttttggac gtgtctggct 420

gtgatctgta tggtgtggac tctgtctgtg gccatggcat ttcccccggt tttagacgtg 480

ggcacttact cattcattag ggaggaagat caatgcacct tccaacaccg ctccttcagg 540

gctaatgatt ccttaggatt tatgctgctt cttgctctca tcctcctagc cacacagctt 600

gtctacctca agctgatatt tttcgtccac gatcgaagaa aaatgaagcc agtccagttt 660

gtagcagcag tcagccagaa ctggactttt catggtcctg gagccagtgg ccaggcagct 720

gccaattggc tagcaggatt tggaaggggt cccacaccac ccaccttgct gggcatcagg 780

caaaatgcaa acaccacagg cagaagaagg ctattggtct tagacgagtt caaaatggag 840

aaaagaatca gcagaatgtt ctatataatg acttttctgt ttctaacctt gtggggcccc 900

tacctggtgg cctgttattg gagagttttt gcaagagggc ctgtagtacc agggggattt 960

ctaacagctg ctgtctggat gagttttgcc caagcaggaa tcaatccttt tgtctgcatt 1020

ttctcaaaca gggagctgag gcgctgtttc agcacaaccc ttctttactg cagaaaatcc 1080

aggttaccaa gggaacctta ctgtgttata tga 1113

<210> 28
<211> 370
<212> PRT
<213> Homo sapiens

<400> 28

Met Ala Asn Tyr Ser His Ala Ala Asp Asn Ile Leu Gln Asn Leu Ser
1 5 10 15

Pro Leu Thr Ala Phe Leu Lys Leu Thr Ser Leu Gly Phe Ile Ile Gly
20 25 30

Val Ser Val Val Gly Asn Leu Leu Ile Ser Ile Leu Leu Val Lys Asp
35 40 45

Lys Thr Leu His Arg Ala Pro Tyr Tyr Phe Leu Leu Asp Leu Cys Cys
50 55 60

Ser Asp Ile Leu Arg Ser Ala Ile Cys Phe Pro Phe Val Phe Asn Ser
65 70 75 80

Val Lys Asn Gly Ser Thr Trp Thr Tyr Gly Thr Leu Thr Cys Lys Val
85 90 95

Ile Ala Phe Leu Gly Val Leu Ser Cys Phe His Thr Ala Phe Met Leu
100 105 110

Phe Cys Ile Ser Val Thr Arg Tyr Leu Ala Ile Ala His His Arg Phe
115 120 125

Tyr Thr Lys Arg Leu Thr Phe Trp Thr Cys Leu Ala Val Ile Cys Met
130 135 140

Val Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Leu Asp Val
145 150 155 160

```
Gly Thr Tyr Ser Phe Ile Arg Glu Glu Asp Gln Cys Thr Phe Gln His
                165                 170                 175

Arg Ser Phe Arg Ala Asn Asp Ser Leu Gly Phe Met Leu Leu Leu Ala
            180                 185                 190

Leu Ile Leu Leu Ala Thr Gln Leu Val Tyr Leu Lys Leu Ile Phe Phe
        195                 200                 205

Val His Asp Arg Arg Lys Met Lys Pro Val Gln Phe Val Ala Ala Val
    210                 215                 220

Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Ser Gly Gln Ala Ala
225                 230                 235                 240

Ala Asn Trp Leu Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Thr Leu
                245                 250                 255

Leu Gly Ile Arg Gln Asn Ala Asn Thr Thr Gly Arg Arg Arg Leu Leu
            260                 265                 270

Val Leu Asp Glu Phe Lys Met Glu Lys Arg Ile Ser Arg Met Phe Tyr
        275                 280                 285

Ile Met Thr Phe Leu Phe Leu Thr Leu Trp Gly Pro Tyr Leu Val Ala
    290                 295                 300

Cys Tyr Trp Arg Val Phe Ala Arg Gly Pro Val Val Pro Gly Gly Phe
305                 310                 315                 320

Leu Thr Ala Ala Val Trp Met Ser Phe Ala Gln Ala Gly Ile Asn Pro
                325                 330                 335

Phe Val Cys Ile Phe Ser Asn Arg Glu Leu Arg Arg Cys Phe Ser Thr
            340                 345                 350

Thr Leu Leu Tyr Cys Arg Lys Ser Arg Leu Pro Arg Glu Pro Tyr Cys
        355                 360                 365

Val Ile
    370
```

<210> 29
<211> 1080
<212> DNA
<213> Homo sapiens

<400> 29
atgcaggtcc cgaacagcac cggcccggac aacgcgacgc tgcagatgct gcggaacccg 60

gcgatcgcgg tggccctgcc cgtggtgtac tcgctggtgg cggcggtcag catcccgggc 120

aacctcttct ctctgtgggt gctgtgccgg cgcatggggc ccagatcccc gtcggtcatc 180

```
ttcatgatca acctgagcgt cacggacctg atgctggcca gcgtgttgcc tttccaaatc    240

tactaccatt gcaaccgcca ccactgggta ttcggggtgc tgctttgcaa cgtggtgacc    300

gtggcctttt acgcaaacat gtattccagc atcctcacca tgacctgtat cagcgtggag    360

cgcttcctgg gggtcctgta cccgctcagc tccaagcgct ggcgccgccg tcgttacgcg    420

gtggccgcgt gtgcagggac ctggctgctg ctcctgaccg ccctgtgccc gctggcgcgc    480

accgatctca cctacccggt gcacgccctg ggcatcatca cctgcttcga cgtcctcaag    540

tggacgatgc tccccagcgt ggccatgtgg gccgtgttcc tcttcaccat cttcatcctg    600

ctgttcctca tcccgttcgt gatcaccgtg gcttgttaca cggccaccat cctcaagctg    660

ttgcgcacgg aggaggcgca cggccgggag cagcggaggc gcgcggtggg cctggccgcg    720

gtggtcttgc tggcctttgt cacctgcttc gcccccaaca acttcgtgct cctggcgcac    780

atcgtgagcc gcctgttcta cggcaagagc tactaccacg tgtacaagct cacgctgtgt    840

ctcagctgcc tcaacaactg tctggacccg tttgtttatt actttgcgtc ccgggaattc    900

cagctgcgcc tgcgggaata tttgggctgc cgccgggtgc ccagagacac cctggacacg    960

cgccgcgaga gcctcttctc cgccaggacc acgtccgtgc gctccgaggc cggtgcgcac   1020

cctgaaggga tggagggagc caccaggccc ggcctccaga ggcaggagag tgtgttctga   1080
```

<210> 30
<211> 359
<212> PRT
<213> Homo sapiens

<400> 30

```
Met Gln Val Pro Asn Ser Thr Gly Pro Asp Asn Ala Thr Leu Gln Met
1               5                  10                  15

Leu Arg Asn Pro Ala Ile Ala Val Ala Leu Pro Val Val Tyr Ser Leu
            20                  25                  30

Val Ala Ala Val Ser Ile Pro Gly Asn Leu Phe Ser Leu Trp Val Leu
        35                  40                  45

Cys Arg Arg Met Gly Pro Arg Ser Pro Ser Val Ile Phe Met Ile Asn
    50                  55                  60

Leu Ser Val Thr Asp Leu Met Leu Ala Ser Val Leu Pro Phe Gln Ile
65                  70                  75                  80

Tyr Tyr His Cys Asn Arg His His Trp Val Phe Gly Val Leu Leu Cys
                85                  90                  95

Asn Val Val Thr Val Ala Phe Tyr Ala Asn Met Tyr Ser Ser Ile Leu
            100                 105                 110

Thr Met Thr Cys Ile Ser Val Glu Arg Phe Leu Gly Val Leu Tyr Pro
        115                 120                 125
```

```
Leu Ser Ser Lys Arg Trp Arg Arg Arg Tyr Ala Val Ala Ala Cys
    130                 135                 140

Ala Gly Thr Trp Leu Leu Leu Leu Thr Ala Leu Cys Pro Leu Ala Arg
145                 150                 155                 160

Thr Asp Leu Thr Tyr Pro Val His Ala Leu Gly Ile Ile Thr Cys Phe
                165                 170                 175

Asp Val Leu Lys Trp Thr Met Leu Pro Ser Val Ala Met Trp Ala Val
            180                 185                 190

Phe Leu Phe Thr Ile Phe Ile Leu Leu Phe Leu Ile Pro Phe Val Ile
        195                 200                 205

Thr Val Ala Cys Tyr Thr Ala Thr Ile Leu Lys Leu Leu Arg Thr Glu
    210                 215                 220

Glu Ala His Gly Arg Glu Gln Arg Arg Arg Ala Val Gly Leu Ala Ala
225                 230                 235                 240

Val Val Leu Leu Ala Phe Val Thr Cys Phe Ala Pro Asn Asn Phe Val
                245                 250                 255

Leu Leu Ala His Ile Val Ser Arg Leu Phe Tyr Gly Lys Ser Tyr Tyr
            260                 265                 270

His Val Tyr Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu
        275                 280                 285

Asp Pro Phe Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu
    290                 295                 300

Arg Glu Tyr Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr
305                 310                 315                 320

Arg Arg Glu Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu
                325                 330                 335

Ala Gly Ala His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu
            340                 345                 350

Gln Arg Gln Glu Ser Val Phe
        355
```

<210> 31
<211> 1503
<212> DNA
<213> Homo sapiens

<400> 31

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atggagcgtc cctgggagga cagcccaggc ccggaggggg cagctgaggg ctcgcctgtg     60

ccagtcgccg ccggggcgcg ctccggtgcc gcggcgagtg gcacaggctg gcagccatgg    120
```

```
gctgagtgcc cgggacccaa ggggaggggg caactgctgg cgaccgccgg ccctttgcgt    180

cgctggcccg ccccctcgcc tgccagctcc agccccgccc ccggagcggc gtccgctcac    240

tcggttcaag gcagcgcgac tgcgggtggc gcacgaccag ggcgcagacc ttggggcgcg    300

cggcccatgg agtcggggct gctgcggccg gcgccggtga gcgaggtcat cgtcctgcat    360

tacaactaca ccggcaagct ccgcggtgcg agctaccagc cgggtgccgg cctgcgcgcc    420

gacgccgtgg tgtgcctggc ggtgtgcgcc ttcatcgtgc tagagaatct agccgtgttg    480

ttggtgctcg gacgccaccc gcgcttccac gctcccatgt tcctgctcct gggcagcctc    540

acgttgtcgg atctgctggc aggcgccgcc tacgccgcca acatcctact gtcggggccg    600

ctcacgctga aactgtcccc cgcgctctgg ttcgcacggg agggaggcgt cttcgtggca    660

ctcactgcgt ccgtgctgag cctcctggcc atcgcgctgg agcgcagcct caccatggcg    720

cgcagggggc ccgcgcccgt ctccagtcgg gggcgcacgc tggcgatggc agccgcggcc    780

tggggcgtgt cgctgctcct cgggctcctg ccagcgctgg gctggaattg cctgggtcgc    840

ctggacgctt gctccactgt cttgccgctc tacgccaagg cctacgtgct cttctgcgtg    900

ctcgccttcg tgggcatcct ggccgcgatc tgtgcactct acgcgcgcat ctactgccag    960

gtacgcgcca acgcgcggcg cctgccggca cggcccggga ctgcggggac cacctcgacc   1020

cgggcgcgtc gcaagccgcg ctctctggcc ttgctgcgca cgctcagcgt ggtgctcctg   1080

gcctttgtgg catgttgggg ccccctcttc ctgctgctgt tgctcgacgt ggcgtgcccg   1140

gcgcgcacct gtcctgtact cctgcaggcc gatcccttcc tgggactggc catggccaac   1200

tcacttctga accccatcat ctacacgctc accaaccgcg acctgcgcca cgcgctcctg   1260

cgcctggtct gctgcggacg ccactcctgc ggcagagacc cgagtggctc ccagcagtcg   1320

gcgagcgcgg ctgaggcttc cgggggcctg cgccgctgcc tgcccccggg ccttgatggg   1380

agcttcagcg gctcggagcg ctcatcgccc cagcgcgacg ggctggacac cagcggctcc   1440

acaggcagcc ccggtgcacc cacagccgcc cggactctgg tatcagaacc ggctgcagac   1500

tga                                                                 1503
```

<210> 32
<211> 500
<212> PRT
<213> Homo sapiens

<400> 32

```
Met Glu Arg Pro Trp Glu Asp Ser Pro Gly Pro Glu Gly Ala Ala Glu
1               5                  10                  15

Gly Ser Pro Val Pro Val Ala Ala Gly Ala Arg Ser Gly Ala Ala Ala
            20                  25                  30

Ser Gly Thr Gly Trp Gln Pro Trp Ala Glu Cys Pro Gly Pro Lys Gly
        35                  40                  45

Arg Gly Gln Leu Leu Ala Thr Ala Gly Pro Leu Arg Arg Trp Pro Ala
    50                  55                  60
```

```
Pro Ser Pro Ala Ser Ser Ser Pro Ala Pro Gly Ala Ala Ser Ala His
65                  70                  75                  80

Ser Val Gln Gly Ser Ala Thr Ala Gly Gly Ala Arg Pro Gly Arg Arg
                85                  90                  95

Pro Trp Gly Ala Arg Pro Met Glu Ser Gly Leu Leu Arg Pro Ala Pro
            100                 105                 110

Val Ser Glu Val Ile Val Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg
        115                 120                 125

Gly Ala Ser Tyr Gln Pro Gly Ala Gly Leu Arg Ala Asp Ala Val Val
    130                 135                 140

Cys Leu Ala Val Cys Ala Phe Ile Val Leu Glu Asn Leu Ala Val Leu
145                 150                 155                 160

Leu Val Leu Gly Arg His Pro Arg Phe His Ala Pro Met Phe Leu Leu
                165                 170                 175

Leu Gly Ser Leu Thr Leu Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala
            180                 185                 190

Ala Asn Ile Leu Leu Ser Gly Pro Leu Thr Leu Lys Leu Ser Pro Ala
        195                 200                 205

Leu Trp Phe Ala Arg Glu Gly Gly Val Phe Val Ala Leu Thr Ala Ser
    210                 215                 220

Val Leu Ser Leu Leu Ala Ile Ala Leu Glu Arg Ser Leu Thr Met Ala
225                 230                 235                 240

Arg Arg Gly Pro Ala Pro Val Ser Ser Arg Gly Arg Thr Leu Ala Met
                245                 250                 255

Ala Ala Ala Ala Trp Gly Val Ser Leu Leu Leu Gly Leu Leu Pro Ala
            260                 265                 270

Leu Gly Trp Asn Cys Leu Gly Arg Leu Asp Ala Cys Ser Thr Val Leu
        275                 280                 285

Pro Leu Tyr Ala Lys Ala Tyr Val Leu Phe Cys Val Leu Ala Phe Val
    290                 295                 300

Gly Ile Leu Ala Ala Ile Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln
305                 310                 315                 320

Val Arg Ala Asn Ala Arg Arg Leu Pro Ala Arg Pro Gly Thr Ala Gly
                325                 330                 335
```

```
Thr Thr Ser Thr Arg Ala Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu
            340                 345                 350

Arg Thr Leu Ser Val Val Leu Leu Ala Phe Val Ala Cys Trp Gly Pro
        355                 360                 365

Leu Phe Leu Leu Leu Leu Leu Asp Val Ala Cys Pro Ala Arg Thr Cys
    370                 375                 380

Pro Val Leu Leu Gln Ala Asp Pro Phe Leu Gly Leu Ala Met Ala Asn
385                 390                 395                 400

Ser Leu Leu Asn Pro Ile Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg
                405                 410                 415

His Ala Leu Leu Arg Leu Val Cys Cys Gly Arg His Ser Cys Gly Arg
            420                 425                 430

Asp Pro Ser Gly Ser Gln Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly
        435                 440                 445

Gly Leu Arg Arg Cys Leu Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly
    450                 455                 460

Ser Glu Arg Ser Ser Pro Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser
465                 470                 475                 480

Thr Gly Ser Pro Gly Ala Pro Thr Ala Ala Arg Thr Leu Val Ser Glu
                485                 490                 495

Pro Ala Ala Asp
            500
```

<210> 33
<211> 1029
<212> DNA
<213> Homo sapiens

<400> 33

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atgcaagccg tcgacaatct cacctctgcg cctgggaaca ccagtctgtg caccagagac     60

tacaaaatca cccaggtcct cttcccactg ctctacactg tcctgttttt tgttggactt    120

atcacaaatg gcctggcgat gaggattttc tttcaaatcc ggagtaaatc aaactttatt    180

atttttctta agaacacagt catttctgat cttctcatga ttctgacttt tccattcaaa    240

attcttagtg atgccaaact gggaacagga ccactgagaa cttttgtgtg tcaagttacc    300

tccgtcatat tttatttcac aatgtatatc agtatttcat tcctgggact gataactatc    360

gatcgctacc agaagaccac caggccattt aaaacatcca accccaaaaa tctcttgggg    420

gctaagattc tctctgttgt catctgggca ttcatgttct tactctcttt gcctaacatg    480

attctgacca acaggcagcc gagagacaag aatgtgaaga aatgctcttt ccttaaatca    540

gagttcggtc tagtctggca tgaaatagta aattacatct gtcaagtcat tttctggatt    600
```

aatttcttaa ttgttattgt atgttataca ctcattacaa aagaactgta ccggtcatac 660

gtaagaacga ggggtgtagg taaagtcccc aggaaaaagg tgaacgtcaa agttttcatt 720

atcattgctg tattctttat ttgttttgtt cctttccatt ttgcccgaat tccttacacc 780

ctgagccaaa cccgggatgt ctttgactgc actgctgaaa atactctgtt ctatgtgaaa 840

gagagcactc tgtggttaac ttccttaaat gcatgcctgg atccgttcat ctatttttc 900

ctttgcaagt ccttcagaaa ttccttgata agtatgctga agtgccccaa ttctgcaaca 960

tctctgtccc aggacaatag gaaaaaagaa caggatggtg gtgacccaaa tgaagagact 1020

ccaatgtaa 1029

<210> 34
<211> 342
<212> PRT
<213> Homo sapiens

<400> 34

Met Gln Ala Val Asp Asn Leu Thr Ser Ala Pro Gly Asn Thr Ser Leu
1 5 10 15

Cys Thr Arg Asp Tyr Lys Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr
20 25 30

Thr Val Leu Phe Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg
35 40 45

Ile Phe Phe Gln Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys
50 55 60

Asn Thr Val Ile Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys
65 70 75 80

Ile Leu Ser Asp Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val
85 90 95

Cys Gln Val Thr Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile
100 105 110

Ser Phe Leu Gly Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg
115 120 125

Pro Phe Lys Thr Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu
130 135 140

Ser Val Val Ile Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met
145 150 155 160

Ile Leu Thr Asn Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser
165 170 175

Phe Leu Lys Ser Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr
180 185 190

Ile Cys Gln Val Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys
195 200 205

Tyr Thr Leu Ile Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg
210 215 220

Gly Val Gly Lys Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile
225 230 235 240

Ile Ile Ala Val Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg
245 250 255

Ile Pro Tyr Thr Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala
260 265 270

Glu Asn Thr Leu Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser
275 280 285

Leu Asn Ala Cys Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser
290 295 300

Phe Arg Asn Ser Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr
305 310 315 320

Ser Leu Ser Gln Asp Asn Arg Lys Lys Glu Gln Asp Gly Gly Asp Pro
325 330 335

Asn Glu Glu Thr Pro Met
340

<210> 35
<211> 1077
<212> DNA
<213> Homo sapiens

<400> 35
atgtcggtct gctaccgtcc cccagggaac gagacactgc tgagctggaa gacttcgcgg 60

gccacaggca cagccttcct gctgctggcg gcgctgctgg ggctgcctgg caacggcttc 120

gtggtgtgga gcttggcggg ctggcggcct gcacgggggc gaccgctggc ggccacgctt 180

gtgctgcacc tggcgctggc cgacggcgcg gtgctgctgc tcacgccgct ctttgtggcc 240

ttcctgaccc ggcaggcctg gccgctgggc caggcgggct gcaaggcggt gtactacgtg 300

tgcgcgctca gcatgtacgc cagcgtgctg ctcaccggcc tgctcagcct gcagcgctgc 360

ctcgcagtca cccgcccctt cctggcgcct cggctgcgca gcccggccct ggcccgccgc 420

ctgctgctgg cggtctggct ggccgccctg ttgctcgccg tcccggccgc cgtctaccgc 480

cacctgtgga gggaccgcgt atgccagctg tgccacccgt cgccggtcca cgccgccgcc 540

cacctgagcc tggagactct gaccgctttc gtgcttcctt tcgggctgat gctcggctgc 600

tacagcgtga cgctggcacg gctgcggggc gcccgctggg gctccgggcg gcacggggcg 660

cgggtgggcc ggctggtgag cgccatcgtg cttgccttcg gcttgctctg ggcccccctac 720

cacgcagtca accttctgca ggcggtcgca gcgctggctc caccggaagg ggccttggcg 780

aagctgggcg gagccggcca ggcggcgcga gcgggaacta cggccttggc cttcttcagt 840

tctagcgtca acccggtgct ctacgtcttc accgctggag atctgctgcc ccgggcaggt 900

ccccgtttcc tcacgcggct cttcgaaggc tctggggagg cccgaggggg cggccgctct 960

agggaaggga ccatggagct ccgaactacc cctcagctga aagtggtggg gcagggccgc 1020

ggcaatggag acccgggggg tgggatggag aaggacggtc cggaatggga cctttga 1077

<210> 36
<211> 358
<212> PRT
<213> Homo sapiens

<400> 36

Met Ser Val Cys Tyr Arg Pro Pro Gly Asn Glu Thr Leu Leu Ser Trp
1 5 10 15

Lys Thr Ser Arg Ala Thr Gly Thr Ala Phe Leu Leu Leu Ala Ala Leu
20 25 30

Leu Gly Leu Pro Gly Asn Gly Phe Val Val Trp Ser Leu Ala Gly Trp
35 40 45

Arg Pro Ala Arg Gly Arg Pro Leu Ala Ala Thr Leu Val Leu His Leu
50 55 60

Ala Leu Ala Asp Gly Ala Val Leu Leu Leu Thr Pro Leu Phe Val Ala
65 70 75 80

Phe Leu Thr Arg Gln Ala Trp Pro Leu Gly Gln Ala Gly Cys Lys Ala
85 90 95

Val Tyr Tyr Val Cys Ala Leu Ser Met Tyr Ala Ser Val Leu Leu Thr
100 105 110

Gly Leu Leu Ser Leu Gln Arg Cys Leu Ala Val Thr Arg Pro Phe Leu
115 120 125

Ala Pro Arg Leu Arg Ser Pro Ala Leu Ala Arg Arg Leu Leu Leu Ala
130 135 140

Val Trp Leu Ala Ala Leu Leu Leu Ala Val Pro Ala Ala Val Tyr Arg
145 150 155 160

His Leu Trp Arg Asp Arg Val Cys Gln Leu Cys His Pro Ser Pro Val
165 170 175

His Ala Ala Ala His Leu Ser Leu Glu Thr Leu Thr Ala Phe Val Leu
180 185 190

```
Pro Phe Gly Leu Met Leu Gly Cys Tyr Ser Val Thr Leu Ala Arg Leu
        195                 200                 205

Arg Gly Ala Arg Trp Gly Ser Gly Arg His Gly Ala Arg Val Gly Arg
    210                 215                 220

Leu Val Ser Ala Ile Val Leu Ala Phe Gly Leu Leu Trp Ala Pro Tyr
225                 230                 235                 240

His Ala Val Asn Leu Leu Gln Ala Val Ala Ala Leu Ala Pro Pro Glu
                245                 250                 255

Gly Ala Leu Ala Lys Leu Gly Gly Ala Gly Gln Ala Ala Arg Ala Gly
            260                 265                 270

Thr Thr Ala Leu Ala Phe Phe Ser Ser Ser Val Asn Pro Val Leu Tyr
        275                 280                 285

Val Phe Thr Ala Gly Asp Leu Leu Pro Arg Ala Gly Pro Arg Phe Leu
    290                 295                 300

Thr Arg Leu Phe Glu Gly Ser Gly Glu Ala Arg Gly Gly Gly Arg Ser
305                 310                 315                 320

Arg Glu Gly Thr Met Glu Leu Arg Thr Thr Pro Gln Leu Lys Val Val
                325                 330                 335

Gly Gln Gly Arg Gly Asn Gly Asp Pro Gly Gly Gly Met Glu Lys Asp
            340                 345                 350

Gly Pro Glu Trp Asp Leu
        355
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<210> 37
<211> 1005
<212> DNA
<213> Homo sapiens

<400> 37

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atgctgggga tcatggcatg gaatgcaact tgcaaaaact ggctggcagc agaggctgcc     60

ctggaaaagt actacctttc catttttat gggattgagt tcgttgtggg agtccttgga    120

aataccattg ttgtttacgg ctacatcttc tctctgaaga actggaacag cagtaatatt    180

tatctcttta acctctctgt ctctgactta gcttttctgt gcaccctccc catgctgata    240

aggagttatg ccaatggaaa ctggatatat ggagacgtgc tctgcataag caaccgatat    300

gtgcttcatg ccaacctcta taccagcatt ctctttctca cttttatcag catagatcga    360

tacttgataa ttaagtatcc tttccgagaa caccttctgc aaaagaaaga gtttgctatt    420

ttaatctcct tggccatttg ggttttagta accttagagt tactacccat acttcccctt    480

ataaatcctg ttataactga caatggcacc acctgtaatg attttgcaag ttctggagac    540

cccaactaca acctcattta cagcatgtgt ctaacactgt tggggttcct tattcctctt    600
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tttgtgatgt gtttctttta ttacaagatt gctctcttcc taaagcagag gaataggcag 660

gttgctactg ctctgcccct tgaaaagcct ctcaacttgg tcatcatggc agtggtaatc 720

ttctctgtgc tttttacacc ctatcacgtc atgcggaatg tgaggatcgc ttcacgcctg 780

gggagttgga agcagtatca gtgcactcag gtcgtcatca actcctttta cattgtgaca 840

cggcctttgg cctttctgaa cagtgtcatc aaccctgtct tctattttct tttgggagat 900

cacttcaggg acatgctgat gaatcaactg agacacaact tcaaatccct tacatccttt 960

agcagatggg ctcatgaact cctactttca ttcagagaaa agtga 1005

<210> 38
<211> 334
<212> PRT
<213> Homo sapiens

<400> 38

Met Leu Gly Ile Met Ala Trp Asn Ala Thr Cys Lys Asn Trp Leu Ala
1 5 10 15

Ala Glu Ala Ala Leu Glu Lys Tyr Tyr Leu Ser Ile Phe Tyr Gly Ile
20 25 30

Glu Phe Val Val Gly Val Leu Gly Asn Thr Ile Val Val Tyr Gly Tyr
35 40 45

Ile Phe Ser Leu Lys Asn Trp Asn Ser Ser Asn Ile Tyr Leu Phe Asn
50 55 60

Leu Ser Val Ser Asp Leu Ala Phe Leu Cys Thr Leu Pro Met Leu Ile
65 70 75 80

Arg Ser Tyr Ala Asn Gly Asn Trp Ile Tyr Gly Asp Val Leu Cys Ile
85 90 95

Ser Asn Arg Tyr Val Leu His Ala Asn Leu Tyr Thr Ser Ile Leu Phe
100 105 110

Leu Thr Phe Ile Ser Ile Asp Arg Tyr Leu Ile Ile Lys Tyr Pro Phe
115 120 125

Arg Glu His Leu Leu Gln Lys Lys Glu Phe Ala Ile Leu Ile Ser Leu
130 135 140

Ala Ile Trp Val Leu Val Thr Leu Glu Leu Leu Pro Ile Leu Pro Leu
145 150 155 160

Ile Asn Pro Val Ile Thr Asp Asn Gly Thr Thr Cys Asn Asp Phe Ala
165 170 175

Ser Ser Gly Asp Pro Asn Tyr Asn Leu Ile Tyr Ser Met Cys Leu Thr
180 185 190

Leu Leu Gly Phe Leu Ile Pro Leu Phe Val Met Cys Phe Phe Tyr Tyr
195 200 205

Lys Ile Ala Leu Phe Leu Lys Gln Arg Asn Arg Gln Val Ala Thr Ala
210 215 220

Leu Pro Leu Glu Lys Pro Leu Asn Leu Val Ile Met Ala Val Val Ile
225 230 235 240

Phe Ser Val Leu Phe Thr Pro Tyr His Val Met Arg Asn Val Arg Ile
245 250 255

Ala Ser Arg Leu Gly Ser Trp Lys Gln Tyr Gln Cys Thr Gln Val Val
260 265 270

Ile Asn Ser Phe Tyr Ile Val Thr Arg Pro Leu Ala Phe Leu Asn Ser
275 280 285

Val Ile Asn Pro Val Phe Tyr Phe Leu Leu Gly Asp His Phe Arg Asp
290 295 300

Met Leu Met Asn Gln Leu Arg His Asn Phe Lys Ser Leu Thr Ser Phe
305 310 315 320

Ser Arg Trp Ala His Glu Leu Leu Leu Ser Phe Arg Glu Lys
325 330

<210> 39
<211> 1296
<212> DNA
<213> Homo sapiens

<400> 39
atgcaggcgc ttaacattac cccggagcag ttctctcggc tgctgcggga ccacaacctg 60

acgcgggagc agttcatcgc tctgtaccgg ctgcgaccgc tcgtctacac cccagagctg 120

ccgggacgcg ccaagctggc cctcgtgctc accggcgtgc tcatcttcgc cctggcgctc 180

tttggcaatg ctctggtgtt ctacgtggtg acccgcagca aggccatgcg caccgtcacc 240

aacatcttta tctgctcctt ggcgctcagt gacctgctca tcaccttctt ctgcattccc 300

gtcaccatgc tccagaacat ttccgacaac tggctggggg gtgctttcat ttgcaagatg 360

gtgccatttg tccagtctac cgctgttgtg acagaaatgc tcactatgac ctgcattgct 420

gtggaaaggc accagggact tgtgcatcct tttaaaatga agtggcaata caccaaccga 480

agggctttca caatgctagg tgtggtctgg ctggtggcag tcatcgtagg atcacccatg 540

tggcacgtgc aacaacttga gatcaaatat gacttcctat atgaaaagga acacatctgc 600

tgcttagaag agtggaccag ccctgtgcac cagaagatct acaccacctt catccttgtc 660

atcctcttcc tcctgcctct tatggtgatg cttattctgt acagtaaaat tggttatgaa 720

ctttggataa agaaaagagt tggggatggt tcagtgcttc gaactattca tggaaaagaa 780

atgtccaaaa tagccaggaa gaagaaacga gctgtcatta tgatggtgac agtggtggct 840

ctctttgctg tgtgctgggc accattccat gttgtccata tgatgattga atacagtaat 900

tttgaaaagg aatatgatga tgtcacaatc aagatgattt ttgctatcgt gcaaattatt 960

ggattttcca actccatctg taatcccatt gtctatgcat ttatgaatga aaacttcaaa 1020

aaaaatgttt tgtctgcagt ttgttattgc atagtaaata aaaccttctc tccagcacaa 1080

aggcatggaa attcaggaat tacaatgatg cggaagaaag caaagttttc cctcagagag 1140

aatccagtgg aggaaaccaa aggagaagca ttcagtgatg gcaacattga agtcaaattg 1200

tgtgaacaga cagaggagaa gaaaaagctc aaacgacatc ttgctctctt taggtctgaa 1260

ctggctgaga attctccttt agacagtggg cattaa 1296

<210> 40
<211> 431
<212> PRT
<213> Homo sapiens

<400> 40

Met Gln Ala Leu Asn Ile Thr Pro Glu Gln Phe Ser Arg Leu Leu Arg
1 5 10 15

Asp His Asn Leu Thr Arg Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg
20 25 30

Pro Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu
35 40 45

Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala
50 55 60

Leu Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr
65 70 75 80

Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe
85 90 95

Phe Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Asn Trp Leu
100 105 110

Gly Gly Ala Phe Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala
115 120 125

Val Val Thr Glu Met Leu Thr Met Thr Cys Ile Ala Val Glu Arg His
130 135 140

Gln Gly Leu Val His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg
145 150 155 160

Arg Ala Phe Thr Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val
165 170 175

Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe
180 185 190

```
Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro
        195                 200                 205

Val His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu
    210                 215                 220

Leu Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile Gly Tyr Glu
225                 230                 235                 240

Leu Trp Ile Lys Lys Arg Val Gly Asp Gly Ser Val Leu Arg Thr Ile
                245                 250                 255

His Gly Lys Glu Met Ser Lys Ile Ala Arg Lys Lys Lys Arg Ala Val
            260                 265                 270

Ile Met Met Val Thr Val Val Ala Leu Phe Ala Val Cys Trp Ala Pro
        275                 280                 285

Phe His Val Val His Met Met Ile Glu Tyr Ser Asn Phe Glu Lys Glu
    290                 295                 300

Tyr Asp Asp Val Thr Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile
305                 310                 315                 320

Gly Phe Ser Asn Ser Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn
                325                 330                 335

Glu Asn Phe Lys Lys Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val
            340                 345                 350

Asn Lys Thr Phe Ser Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr
        355                 360                 365

Met Met Arg Lys Lys Ala Lys Phe Ser Leu Arg Glu Asn Pro Val Glu
    370                 375                 380

Glu Thr Lys Gly Glu Ala Phe Ser Asp Gly Asn Ile Glu Val Lys Leu
385                 390                 395                 400

Cys Glu Gln Thr Glu Glu Lys Lys Lys Leu Lys Arg His Leu Ala Leu
                405                 410                 415

Phe Arg Ser Glu Leu Ala Glu Asn Ser Pro Leu Asp Ser Gly His
            420                 425                 430
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<210> 41
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 41
ctgtgtacag cagttcgcag agtg 24

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 42
gagtgccagg cagagcaggt agac 24

<210> 43
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 43
cccgaattcc tgcttgctcc cagcttggcc c 31

<210> 44
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 44
tgtggatcct gctgtcaaag gtcccattcc gg 32

<210> 45
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 45
tcacaatgct aggtgtggtc 20

<210> 46
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 46
tgcatagaca atgggattac ag 22

<210> 47
<211> 511
<212> DNA
<213> Homo sapiens

<400> 47

tcacaatgct aggtgtggtc tggctggtgg cagtcatcgt aggatcaccc atgtggcacg 60

tgcaacaact tgagatcaaa tatgacttcc tatatgaaaa ggaacacatc tgctgcttag 120

aagagtggac cagccctgtg caccagaaga tctacaccac cttcatcctt gtcatcctct 180

tcctcctgcc tcttatggtg atgcttattc tgtacgtaaa attggttatg aactttggat 240

aaagaaaaga gttggggatg gttcagtgct tcgaactatt catggaaaag aaatgtccaa 300

aatagccagg aagaagaaac gagctgtcat tatgatggtg acagtggtgg ctctctttgc 360

tgtgtgctgg gcaccattcc atgttgtcca tatgatgatt gaatacagta attttgaaaa 420

ggaatatgat gatgtcacaa tcaagatgat ttttgctatc gtgcaaatta ttggattttc 480

caactccatc tgtaatccca ttgtctatgc a 511

<210> 48
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 48
ctgcttagaa gagtggacca g 21

<210> 49
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 49
ctgtgcacca gaagatctac ac 22

<210> 50
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 50
caaggatgaa ggtggtgtag a 21

<210> 51
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 51
gtgtagatct tctggtgcac agg 23

<210> 52
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 52
gcaatgcagg tcatagtgag c 21

<210> 53
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 53
tggagcatgg tgacgggaat gcagaag 27

<210> 54
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 54
gtgatgagca ggtcactgag cgccaag 27

<210> 55
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 55
gcaatgcagg cgcttaacat tac 23

<210> 56
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 56
ttgggttaca atctgaaggg ca 22

<210> 57
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 57
actccgtgtc cagcaggact ctg 23

<210> 58

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 58
tgcgtgttcc tggaccctca cgtg 24

<210> 59
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 59
caggccttgg attttaatgt cagggatgg 29

<210> 60
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 60
ggagagtcag ctctgaaaga attcagg 27

<210> 61
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 61
tgatgtgatg ccagatacta atagcac 27

<210> 62
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 62
cctgattcat ttaggtgaga ttgagac 27

<210> 63
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 63
cccaagcttc cccaggtgta tttgat 26

<210> 64
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 64
gttggatcca cataatgcat tttctc 26

<210> 65
<211> 1080
<212> DNA
<213> Homo sapiens

<400> 65
atgattctca actcttctac tgaagatggt attaaaagaa tccaagatga ttgtcccaaa 60

gctggaaggc ataattacat atttgtcatg attcctactt tatacagtat catctttgtg 120

gtgggaatat ttggaaacag cttggtggtg atagtcattt acttttatat gaagctgaag 180

actgtggcca gtgtttttct tttgaattta gcactggctg acttatgctt tttactgact 240

ttgccactat gggctgtcta cacagctatg gaataccgct ggccctttgg caattaccta 300

tgtaagattg cttcagccag cgtcagtttc aacctgtacg ctagtgtgtt tctactcacg 360

tgtctcagca ttgatcgata cctggctatt gttcacccaa tgaagtcccg ccttcgacgc 420

acaatgcttg tagccaaagt cacctgcatc atcatttggc tgctggcagg cttggccagt 480

ttgccagcta taatccatcg aaatgtattt ttcattgaga acaccaatat tacagtttgt 540

gctttccatt atgagtccca aaattcaacc cttccgatag ggctgggcct gaccaaaaat 600

atactgggtt tcctgtttcc ttttctgatc attcttacaa gttatactct tatttggaag 660

gccctaaaga aggcttatga aattcagaag aacaaaccaa gaaatgatga tatttttaag 720

ataattatgg caattgtgct tttctttttc ttttcctgga ttccccacca aatattcact 780

tttctggatg tattgattca actaggcatc atacgtgact gtagaattgc agatattgtg 840

gacacggcca tgcctatcac catttgtata gcttatttta acaattgcct gaatcctctt 900

ttttatggct ttctggggaa aaaatttaaa agatattttc tccagcttct aaaatatatt 960

cccccaaaag ccaaatccca ctcaaacctt tcaacaaaaa tgagcacgct ttcctaccgc 1020

ccctcagata atgtaagctc atccaccaag aagcctgcac catgttttga ggttgagtga 1080

<210> 66
<211> 359
<212> PRT
<213> Homo sapiens

<400> 66

Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp
1 5 10 15

Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro
20 25 30

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Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu
        35                  40                  45

Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser
    50                  55                  60

Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr
65                  70                  75                  80

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe
                85                  90                  95

Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu
            100                 105                 110

Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu
        115                 120                 125

Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val
    130                 135                 140

Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser
145                 150                 155                 160

Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn
                165                 170                 175

Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro
            180                 185                 190

Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe
        195                 200                 205

Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys
    210                 215                 220

Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys
225                 230                 235                 240

Ile Ile Met Ala Ile Val Leu Phe Phe Phe Phe Ser Trp Ile Pro His
                245                 250                 255

Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg
            260                 265                 270

Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile
        275                 280                 285

Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe
    290                 295                 300

Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile
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305 310 315 320

Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr
325 330 335

Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro
340 345 350

Ala Pro Cys Phe Glu Val Glu
355

<210> 67
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 67
accatgggca gcccctggaa cggcagc 27

<210> 68
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 68
agaaccacca ccagcaggac gcggacggtc tgccggtgg 39

<210> 69
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 69
gtccgcgtcc tgctggtggt ggttctggca tttataatt 39

<210> 70
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 70
cctggatcct tatcccatcg tcttcacgtt agc 33

<210> 71
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 71
ctggaattct cctgccagca tggtga 26

<210> 72
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 72
gcaggatcct atattgcgtg ctctgtcccc 30

<210> 73
<211> 999
<212> DNA
<213> Homo sapiens

<400> 73
atggtgaact ccacccaccg tgggatgcac acttctctgc acctctggaa ccgcagcagt 60

tacagactgc acagcaatgc cagtgagtcc cttggaaaag gctactctga tggagggtgc 120

tacgagcaac tttttgtctc tcctgaggtg tttgtgactc tgggtgtcat cagcttgttg 180

gagaatatct tagtgattgt ggcaatagcc aagaacaaga atctgcattc acccatgtac 240

tttttcatct gcagcttggc tgtggctgat atgctggtga gcgtttcaaa tggatcagaa 300

accattatca tcaccctatt aaacagtaca gatacggatg cacagagttt cacagtgaat 360

attgataatg tcattgactc ggtgatctgt agctccttgc ttgcatccat ttgcagcctg 420

ctttcaattg cagtggacag gtactttact atcttctatg ctctccagta ccataacatt 480

atgacagtta agcgggttgg gatcagcata agttgtatct gggcagcttg cacggtttca 540

ggcattttgt tcatcattta ctcagatagt agtgctgtca tcatctgcct catcaccatg 600

ttcttcacca tgctggctct catggcttct ctctatgtcc acatgttcct gatggccagg 660

cttcacatta agaggattgc tgtcctcccc ggcactggtg ccatccgcca aggtgccaat 720

atgaagggag cgattacctt gaccatcctg attggcgtct ttgttgtctg ctgggcccca 780

ttcttcctcc acttaatatt ctacatctct tgtcctcaga atccatattg tgtgtgcttc 840

atgtctcact ttaacttgta tctcatactg atcatgtgta attcaatcat cgatcctctg 900

atttatgcac tccggagtca agaactgagg aaaaccttca aagagatcat ctgttgctat 960

cccctgggag gcctttgtga cttgtctagc agatattaa 999

<210> 74
<211> 332
<212> PRT
<213> Homo sapiens

<400> 74

Met Val Asn Ser Thr His Arg Gly Met His Thr Ser Leu His Leu Trp
1 5 10 15

Asn Arg Ser Ser Tyr Arg Leu His Ser Asn Ala Ser Glu Ser Leu Gly

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            20                  25                  30

Lys Gly Tyr Ser Asp Gly Gly Cys Tyr Glu Gln Leu Phe Val Ser Pro
        35                  40                  45

Glu Val Phe Val Thr Leu Gly Val Ile Ser Leu Leu Glu Asn Ile Leu
    50                  55                  60

Val Ile Val Ala Ile Ala Lys Asn Lys Asn Leu His Ser Pro Met Tyr
65                  70                  75                  80

Phe Phe Ile Cys Ser Leu Ala Val Ala Asp Met Leu Val Ser Val Ser
                85                  90                  95

Asn Gly Ser Glu Thr Ile Ile Ile Thr Leu Leu Asn Ser Thr Asp Thr
            100                 105                 110

Asp Ala Gln Ser Phe Thr Val Asn Ile Asp Asn Val Ile Asp Ser Val
        115                 120                 125

Ile Cys Ser Ser Leu Leu Ala Ser Ile Cys Ser Leu Leu Ser Ile Ala
    130                 135                 140

Val Asp Arg Tyr Phe Thr Ile Phe Tyr Ala Leu Gln Tyr His Asn Ile
145                 150                 155                 160

Met Thr Val Lys Arg Val Gly Ile Ser Ile Ser Cys Ile Trp Ala Ala
                165                 170                 175

Cys Thr Val Ser Gly Ile Leu Phe Ile Ile Tyr Ser Asp Ser Ser Ala
            180                 185                 190

Val Ile Ile Cys Leu Ile Thr Met Phe Phe Thr Met Leu Ala Leu Met
        195                 200                 205

Ala Ser Leu Tyr Val His Met Phe Leu Met Ala Arg Leu His Ile Lys
    210                 215                 220

Arg Ile Ala Val Leu Pro Gly Thr Gly Ala Ile Arg Gln Gly Ala Asn
225                 230                 235                 240

Met Lys Gly Ala Ile Thr Leu Thr Ile Leu Ile Gly Val Phe Val Val
                245                 250                 255

Cys Trp Ala Pro Phe Phe Leu His Leu Ile Phe Tyr Ile Ser Cys Pro
            260                 265                 270

Gln Asn Pro Tyr Cys Val Cys Phe Met Ser His Phe Asn Leu Tyr Leu
        275                 280                 285

Ile Leu Ile Met Cys Asn Ser Ile Ile Asp Pro Leu Ile Tyr Ala Leu
    290                 295                 300
```

Arg Ser Gln Glu Leu Arg Lys Thr Phe Lys Glu Ile Ile Cys Cys Tyr
305 310 315 320

Pro Leu Gly Gly Leu Cys Asp Leu Ser Ser Arg Tyr
325 330

<210> 75
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 75
ccgaagcttc gagctgagta aggcggcggg ct 32

<210> 76
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 76
gtggaattca tttgccctgc ctcaaccccc a 31

<210> 77
<211> 1344
<212> DNA
<213> Homo sapiens

<400> 77
atggagctgc taaagctgaa ccggagcgtg cagggaaccg gacccgggcc gggggcttcc 60

ctgtgccgcc cgggggcgcc tctcctcaac agcagcagtg tgggcaacct cagctgcgag 120

ccccctcgca ttcgcggagc cgggacacga gaattggagc tggccattag aatcactctt 180

tacgcagtga tcttcctgat gagcgttgga ggaaatatgc tcatcatcgt ggtcctggga 240

ctgagccgcc gcctgaggac tgtcaccaat gccttcctcc tctcactggc agtcagcgac 300

ctcctgctgg ctgtggcttg catgcccttc accctcctgc ccaatctcat gggcacattc 360

atctttggca ccgtcatctg caaggcggtt tcctacctca tgggggtgtc tgtgagtgtg 420

tccacgctaa gcctcgtggc catcgcactg gagcgatata gcgccatctg ccgaccactg 480

caggcacgag tgtggcagac gcgctcccac gcggctcgcg tgattgtagc cacgtggctg 540

ctgtccggac tactcatggt gccctacccc gtgtacactg tcgtgcaacc agtggggcct 600

cgtgtgctgc agtgcgtgca tcgctggccc agtgcgcggg tccgccagac ctggtccgta 660

ctgctgcttc tgctcttgtt cttcatccca ggtgtggtta tggccgtggc ctacgggctt 720

atctctcgcg agctctactt agggcttcgc tttgacggcg acagtgacag cgacagccaa 780

agcagggtcc gaaaccaagg cgggctgcca ggggctgttc accagaacgg gcgttgccgg 840

cctgagactg gcgcggttgg caaagacagc gatggctgct acgtgcaact tccacgttcc 900

cggcctgccc tggagctgac ggcgctgacg gctcctgggc cgggatccgg ctcccggccc 960

acccaggcca agctgctggc taagaagcgc gtggtgcgaa tgttgctggt gatcgttgtg 1020

ctttttttttc tgtgttggtt gccagtttat agtgccaaca cgtggcgcgc ctttgatggc 1080

ccgggtgcac accgagcact ctcgggtgct cctatctcct tcattcactt gctgagctac 1140

gcctcggcct gtgtcaaccc cctggtctac tgcttcatgc accgtcgctt tcgccaggcc 1200

tgcctggaaa cttgcgctcg ctgctgcccc cggcctccac gagctcgccc cagggctctt 1260

cccgatgagg accctcccac tccctccatt gcttcgctgt ccaggcttag ctacaccacc 1320

atcagcacac tgggccctgg ctga 1344

<210> 78
<211> 447
<212> PRT
<213> Homo sapiens

<400> 78

Met Glu Leu Leu Lys Leu Asn Arg Ser Val Gln Gly Thr Gly Pro Gly
1 5 10 15

Pro Gly Ala Ser Leu Cys Arg Pro Gly Ala Pro Leu Leu Asn Ser Ser
20 25 30

Ser Val Gly Asn Leu Ser Cys Glu Pro Pro Arg Ile Arg Gly Ala Gly
35 40 45

Thr Arg Glu Leu Glu Leu Ala Ile Arg Ile Thr Leu Tyr Ala Val Ile
50 55 60

Phe Leu Met Ser Val Gly Gly Asn Met Leu Ile Ile Val Val Leu Gly
65 70 75 80

Leu Ser Arg Arg Leu Arg Thr Val Thr Asn Ala Phe Leu Leu Ser Leu
85 90 95

Ala Val Ser Asp Leu Leu Leu Ala Val Ala Cys Met Pro Phe Thr Leu
100 105 110

Leu Pro Asn Leu Met Gly Thr Phe Ile Phe Gly Thr Val Ile Cys Lys
115 120 125

Ala Val Ser Tyr Leu Met Gly Val Ser Val Ser Val Ser Thr Leu Ser
130 135 140

Leu Val Ala Ile Ala Leu Glu Arg Tyr Ser Ala Ile Cys Arg Pro Leu
145 150 155 160

Gln Ala Arg Val Trp Gln Thr Arg Ser His Ala Ala Arg Val Ile Val
165 170 175

Ala Thr Trp Leu Leu Ser Gly Leu Leu Met Val Pro Tyr Pro Val Tyr
180 185 190

```
Thr Val Val Gln Pro Val Gly Pro Arg Val Leu Gln Cys Val His Arg
        195                 200                 205

Trp Pro Ser Ala Arg Val Arg Gln Thr Trp Ser Val Leu Leu Leu Leu
    210                 215                 220

Leu Leu Phe Phe Ile Pro Gly Val Val Met Ala Val Ala Tyr Gly Leu
225                 230                 235                 240

Ile Ser Arg Glu Leu Tyr Leu Gly Leu Arg Phe Asp Gly Asp Ser Asp
                245                 250                 255

Ser Asp Ser Gln Ser Arg Val Arg Asn Gln Gly Gly Leu Pro Gly Ala
            260                 265                 270

Val His Gln Asn Gly Arg Cys Arg Pro Glu Thr Gly Ala Val Gly Lys
        275                 280                 285

Asp Ser Asp Gly Cys Tyr Val Gln Leu Pro Arg Ser Arg Pro Ala Leu
    290                 295                 300

Glu Leu Thr Ala Leu Thr Ala Pro Gly Pro Gly Ser Gly Ser Arg Pro
305                 310                 315                 320

Thr Gln Ala Lys Leu Leu Ala Lys Lys Arg Val Val Arg Met Leu Leu
                325                 330                 335

Val Ile Val Val Leu Phe Phe Leu Cys Trp Leu Pro Val Tyr Ser Ala
            340                 345                 350

Asn Thr Trp Arg Ala Phe Asp Gly Pro Gly Ala His Arg Ala Leu Ser
        355                 360                 365

Val Ala Pro Ile Ser Phe Ile His Leu Leu Ser Tyr Ala Ser Ala Cys
    370                 375                 380

Val Asn Pro Leu Val Tyr Cys Phe Met His Arg Arg Phe Arg Gln Ala
385                 390                 395                 400

Cys Leu Glu Thr Cys Ala Arg Cys Cys Pro Arg Pro Pro Arg Ala Arg
                405                 410                 415

Pro Arg Ala Leu Pro Asp Glu Asp Pro Pro Thr Pro Ser Ile Ala Ser
            420                 425                 430

Leu Ser Arg Leu Ser Tyr Thr Thr Ile Ser Thr Leu Gly Pro Gly
        435                 440                 445
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<210> 79
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 79
tgcaagctta aaaaggaaaa aatgaacagc 30

<210> 80
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 80
taaggatccc ttcccttcaa aacatccttg 30

<210> 81
<211> 1014
<212> DNA
<213> Homo sapiens

<400> 81
atgaacagca catgtattga agaacagcat gacctggatc actatttgtt tcccattgtt 60

tacatctttg tgattatagt cagcattcca gccaatattg gatctctgtg tgtgtctttc 120

ctgcaaccca agaaggaaag tgaactagga atttacctct tcagtttgtc actatcagat 180

ttactctatg cattaactct ccctttatgg attgattata cttggaataa agacaactgg 240

actttctctc ctgccttgtg caaagggagt gcttttctca tgtacatgaa gttttacagc 300

agcacagcat tcctcacctg cattgccgtt gatcggtatt tggctgttgt ctacccttg 360

aagtttttt tcctaaggac aagaagaatt gcactcatgg tcagcctgtc catctggata 420

ttggaaacca tcttcaatgc tgtcatgttg tgggaagatg aaacagttgt tgaatattgc 480

gatgccgaaa agtctaattt tactttatgc tatgacaaat acccttaga gaaatggcaa 540

atcaacctca acttgttcag gacgtgtaca ggctatgcaa tacctttggt caccatcctg 600

atctgtaacc ggaaagtcta ccaagctgtg cggcacaata aagccacgga aaacaaggaa 660

aagaagagaa tcataaaact acttgtcagc atcacagtta cttttgtctt atgctttact 720

ccctttcatg tgatgttgct gattcgctgc attttagagc atgctgtgaa cttcgaagac 780

cacagcaatt ctgggaagcg aacttacaca atgtatagaa tcacggttgc attaacaagt 840

ttaaattgtg ttgctgatcc aattctgtac tgttttgtta ccgaaacagg aagatatgat 900

atgtggaata tattaaaatt ctgcactggg aggtgtaata catcacaaag acaaagaaaa 960

cgcatacttt ctgtgtctac aaaagatact atggaattag aggtccttga gtag 1014

<210> 82
<211> 337
<212> PRT
<213> Homo sapiens

<400> 82

Met Asn Ser Thr Cys Ile Glu Glu Gln His Asp Leu Asp His Tyr Leu
1 5 10 15

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Phe Pro Ile Val Tyr Ile Phe Val Ile Ile Val Ser Ile Pro Ala Asn
            20                  25                  30

Ile Gly Ser Leu Cys Val Ser Phe Leu Gln Pro Lys Lys Glu Ser Glu
        35                  40                  45

Leu Gly Ile Tyr Leu Phe Ser Leu Ser Leu Ser Asp Leu Leu Tyr Ala
    50                  55                  60

Leu Thr Leu Pro Leu Trp Ile Asp Tyr Thr Trp Asn Lys Asp Asn Trp
65                  70                  75                  80

Thr Phe Ser Pro Ala Leu Cys Lys Gly Ser Ala Phe Leu Met Tyr Met
                85                  90                  95

Lys Phe Tyr Ser Ser Thr Ala Phe Leu Thr Cys Ile Ala Val Asp Arg
            100                 105                 110

Tyr Leu Ala Val Val Tyr Pro Leu Lys Phe Phe Phe Leu Arg Thr Arg
        115                 120                 125

Arg Ile Ala Leu Met Val Ser Leu Ser Ile Trp Ile Leu Glu Thr Ile
    130                 135                 140

Phe Asn Ala Val Met Leu Trp Glu Asp Glu Thr Val Val Glu Tyr Cys
145                 150                 155                 160

Asp Ala Glu Lys Ser Asn Phe Thr Leu Cys Tyr Asp Lys Tyr Pro Leu
                165                 170                 175

Glu Lys Trp Gln Ile Asn Leu Asn Leu Phe Arg Thr Cys Thr Gly Tyr
            180                 185                 190

Ala Ile Pro Leu Val Thr Ile Leu Ile Cys Asn Arg Lys Val Tyr Gln
        195                 200                 205

Ala Val Arg His Asn Lys Ala Thr Glu Asn Lys Glu Lys Lys Arg Ile
    210                 215                 220

Ile Lys Leu Leu Val Ser Ile Thr Val Thr Phe Val Leu Cys Phe Thr
225                 230                 235                 240

Pro Phe His Val Met Leu Leu Ile Arg Cys Ile Leu Glu His Ala Val
                245                 250                 255

Asn Phe Glu Asp His Ser Asn Ser Gly Lys Arg Thr Tyr Thr Met Tyr
            260                 265                 270

Arg Ile Thr Val Ala Leu Thr Ser Leu Asn Cys Val Ala Asp Pro Ile
        275                 280                 285

Leu Tyr Cys Phe Val Thr Glu Thr Gly Arg Tyr Asp Met Trp Asn Ile
```

290 295 300

Leu Lys Phe Cys Thr Gly Arg Cys Asn Thr Ser Gln Arg Gln Arg Lys
305 310 315 320

Arg Ile Leu Ser Val Ser Thr Lys Asp Thr Met Glu Leu Glu Val Leu
325 330 335

Glu

<210> 83
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 83
caggaagaag aaacgagctg tcattatgat ggtgacagtg 40

<210> 84
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 84
cactgtcacc atcataatga cagctcgttt cttcttcctg 40

<210> 85
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 85
ggccaccggc agaccaaacg cgtcctgctg 30

<210> 86
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 86
ctccttcggt cctcctatcg ttgtcagaag t 31

<210> 87
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 87
ggaaaagaag agaatcaaaa aactacttgt cagcatc 37

<210> 88
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 88
ctccttcggt cctcctatcg ttgtcagaag t 31

<210> 89
<211> 1080
<212> DNA
<213> Homo sapiens

<400> 89
atgattctca actcttctac tgaagatggt attaaaagaa tccaagatga ttgtcccaaa 60

gctggaaggc ataattacat atttgtcatg attcctactt tatacagtat catctttgtg 120

gtgggaatat ttggaaacag cttggtggtg atagtcattt acttttatat gaagctgaag 180

actgtggcca gtgtttttct tttgaattta gcactggctg acttatgctt tttactgact 240

ttgccactat gggctgtcta cacagctatg gaataccgct ggccctttgg caattaccta 300

tgtaagattg cttcagccag cgtcagtttc aacctgtacg ctagtgtgtt tctactcacg 360

tgtctcagca ttgatcgata cctggctatt gttcacccaa tgaagtcccg ccttcgacgc 420

acaatgcttg tagccaaagt cacctgcatc atcatttggc tgctggcagg cttggccagt 480

ttgccagcta taatccatcg aaatgtattt ttcattgaga acaccaatat tacagtttgt 540

gctttccatt atgagtccca aaattcaacc cttccgatag ggctgggcct gaccaaaaat 600

atactgggtt tcctgtttcc ttttctgatc attcttacaa gttatactct tatttggaag 660

gccctaaaga aggcttatga aattcagaag aacaaaccaa gaaatgatga tattaaaaag 720

ataattatgg caattgtgct tttctttttc ttttcctgga ttccccacca aatattcact 780

tttctggatg tattgattca actaggcatc atacgtgact gtagaattgc agatattgtg 840

gacacggcca tgcctatcac catttgtata gcttatttta acaattgcct gaatcctctt 900

ttttatggct ttctggggaa aaaatttaaa agatattttc tccagcttct aaaatatatt 960

cccccaaaag ccaaatccca ctcaaacctt tcaacaaaaa tgagcacgct ttcctaccgc 1020

ccctcagata atgtaagctc atccaccaag aagcctgcac catgttttga ggttgagtga 1080

<210> 90
<211> 359
<212> PRT
<213> Homo sapiens

<400> 90

Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp
1 5 10 15

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Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro
            20                  25                  30

Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu
        35                  40                  45

Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser
    50                  55                  60

Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr
65                  70                  75                  80

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe
                85                  90                  95

Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu
            100                 105                 110

Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu
        115                 120                 125

Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val
    130                 135                 140

Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser
145                 150                 155                 160

Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn
                165                 170                 175

Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro
            180                 185                 190

Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe
        195                 200                 205

Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys
    210                 215                 220

Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Lys Lys
225                 230                 235                 240

Ile Ile Met Ala Ile Val Leu Phe Phe Phe Phe Ser Trp Ile Pro His
                245                 250                 255

Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg
            260                 265                 270

Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile
        275                 280                 285

Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe
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290 295 300

Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile
305 310 315 320

Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr
325 330 335

Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro
340 345 350

Ala Pro Cys Phe Glu Val Glu
355

<210> 91
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 91
ccaagaaatg atgatattaa aaagataatt atggc 35

<210> 92
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 92
ctccttcggt cctcctatcg ttgtcagaag t 31

<210> 93
<211> 1080
<212> DNA
<213> Homo sapiens

<400> 93
atgattctca actcttctac tgaagatggt attaaaagaa tccaagatga ttgtcccaaa 60

gctggaaggc ataattacat atttgtcatg attcctactt tatacagtat catctttgtg 120

gtgggaatat ttggaaacag cttggtggtg atagtcattt acttttatat gaagctgaag 180

actgtggcca gtgtttttct tttgaattta gcactggctg acttatgctt tttactgact 240

ttgccactat gggctgtcta cacagctatg gaataccgct ggccctttgg caattaccta 300

tgtaagattg cttcagccag cgtcagtttc gccctgtacg ctagtgtgtt tctactcacg 360

tgtctcagca ttgatcgata cctggctatt gttcacccaa tgaagtcccg ccttcgacgc 420

acaatgcttg tagccaaagt cacctgcatc atcatttggc tgctggcagg cttggccagt 480

ttgccagcta taatccatcg aaatgtattt ttcattgaga acaccaatat tacagtttgt 540

gctttccatt atgagtccca aaattcaacc cttccgatag ggctgggcct gaccaaaaat 600

atactgggtt tcctgtttcc ttttctgatc attcttacaa gttatactct tatttggaag 660

gccctaaaga aggcttatga aattcagaag aacaaaccaa gaaatgatga tatttttaag 720

ataattatgg caattgtgct tttctttttc ttttcctgga ttccccacca aatattcact 780

tttctggatg tattgattca actaggcatc atacgtgact gtagaattgc agatattgtg 840

gacacggcca tgcctatcac catttgtata gcttatttta acaattgcct gaatcctctt 900

ttttatggct ttctggggaa aaaatttaaa agatattttc tccagcttct aaaatatatt 960

cccccaaaag ccaaatccca ctcaaacctt tcaacaaaaa tgagcacgct ttcctaccgc 1020

ccctcagata atgtaagctc atccaccaag aagcctgcac catgttttga ggttgagtga 1080

<210> 94
<211> 359
<212> PRT
<213> Homo sapiens

<400> 94

Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp
1 5 10 15

Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro
20 25 30

Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu
35 40 45

Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser
50 55 60

Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr
65 70 75 80

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe
85 90 95

Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Ala Leu
100 105 110

Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu
115 120 125

Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val
130 135 140

Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser
145 150 155 160

Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn
165 170 175

Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro
180 185 190

```
Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe
        195                 200                 205

Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys
    210                 215                 220

Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys
225                 230                 235                 240

Ile Ile Met Ala Ile Val Leu Phe Phe Phe Phe Ser Trp Ile Pro His
                245                 250                 255

Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg
            260                 265                 270

Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile
        275                 280                 285

Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe
    290                 295                 300

Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile
305                 310                 315                 320

Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr
                325                 330                 335

Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro
            340                 345                 350

Ala Pro Cys Phe Glu Val Glu
        355
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<210> 95
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 95
cccaagcttc cccaggtgta tttgat 26

<210> 96
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 96
cctgcaggcg aaactgactc tggctgaag 29

<210> 97

<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 97
ctgtacgcta gtgtgtttct actcacgtgt ctcagcattg at 42

<210> 98
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 98
gttggatcca cataatgcat tttctc 26

<210> 99
<211> 1080
<212> DNA
<213> Homo sapiens

<400> 99
atgattctca actcttctac tgaagatggt attaaaagaa tccaagatga ttgtcccaaa 60

gctggaaggc ataattacat atttgtcatg attcctactt tatacagtat catctttgtg 120

gtgggaatat ttggaaacag cttggtggtg atagtcattt acttttatat gaagctgaag 180

actgtggcca gtgtttttct tttgaattta gcactggctg acttatgctt tttactgact 240

ttgccactat gggctgtcta cacagctatg gaataccgct ggccctttgg caattaccta 300

tgtaagattg cttcagccag cgtcagtttc aacctgtacg ctagtgtgtt tctactcacg 360

tgtctcagca ttgatcgata cctggctatt gttcacccaa tgaagtcccg ccttcgacgc 420

acaatgcttg tagccaaagt cacctgcatc atcatttggc tgctggcagg cttggccagt 480

ttgccagcta taatccatcg aaatgtattt ttcattgaga acaccaatat tacagtttgt 540

gctttccatt atgagtccca aaattcaacc cttccgatag ggctgggcct gaccaaaaat 600

atactgggtt tcctgtttcc ttttctgatc attcttacaa gttattttgg aattcgaaaa 660

cacttactga agacgaatag ctatgggaag aacaggataa cccgtgacca agttaagaag 720

ataattatgg caattgtgct tttctttttc ttttcctgga ttccccacca aatattcact 780

tttctggatg tattgattca actaggcatc atacgtgact gtagaattgc agatattgtg 840

gacacggcca tgcctatcac catttgtata gcttatttta acaattgcct gaatcctctt 900

ttttatggct ttctggggaa aaaatttaaa agatattttc tccagcttct aaaatatatt 960

cccccaaaag ccaaatccca ctcaaacctt tcaacaaaaa tgagcacgct ttcctaccgc 1020

ccctcagata atgtaagctc atccaccaag aagcctgcac catgttttga ggttgagtga 1080

<210> 100
<211> 359
<212> PRT
<213> Homo sapiens

<400> 100

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Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp
1               5                  10                  15

Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro
            20                  25                  30

Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu
        35                  40                  45

Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser
    50                  55                  60

Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr
65                  70                  75                  80

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe
                85                  90                  95

Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu
            100                 105                 110

Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu
        115                 120                 125

Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val
    130                 135                 140

Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser
145                 150                 155                 160

Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn
                165                 170                 175

Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro
            180                 185                 190

Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe
        195                 200                 205

Leu Ile Ile Leu Thr Ser Tyr Phe Gly Ile Arg Lys His Leu Leu Lys
    210                 215                 220

Thr Asn Ser Tyr Gly Lys Asn Arg Ile Thr Arg Asp Gln Val Lys Lys
225                 230                 235                 240

Ile Ile Met Ala Ile Val Leu Phe Phe Phe Phe Ser Trp Ile Pro His
                245                 250                 255

Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg
            260                 265                 270
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Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile
275 280 285

Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe
290 295 300

Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile
305 310 315 320

Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr
325 330 335

Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro
340 345 350

Ala Pro Cys Phe Glu Val Glu
355

<210> 101
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 101
tccgaattcc aaaataactt gtaagaatga tcagaaa 37

<210> 102
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 102
agatcttaag aagataatta tggcaattgt gct 33

<210> 103
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 103
aattcgaaaa cacttactga agacgaatag ctatgggaag aacaggataa cccgtgacca 60

ag 62

<210> 104
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 104
ttaacttggt cacgggttat cctgttcttc ccatagctat tcgtcttcag taagtgtttt 60

cg 62

<210> 105
<211> 1083
<212> DNA
<213> Homo sapiens

<400> 105
atgattctca actcttctac tgaagatggt attaaaagaa tccaagatga ttgtcccaaa 60

gctggaaggc ataattacat atttgtcatg attcctactt tatacagtat catctttgtg 120

gtgggaatat ttggaaacag cttggtggtg atagtcattt acttttatat gaagctgaag 180

actgtggcca gtgtttttct tttgaattta gcactggctg acttatgctt tttactgact 240

ttgccactat gggctgtcta cacagctatg gaataccgct ggccctttgg caattaccta 300

tgtaagattg cttcagccag cgtcagtttc aacctgtacg ctagtgtgtt tctactcacg 360

tgtctcagca ttgatcgata cctggctatt gttcacccaa tgaagtcccg ccttcgacgc 420

acaatgcttg tagccaaagt cacctgcatc atcatttggc tgctggcagg cttggccagt 480

ttgccagcta taatccatcg aaatgtattt ttcattgaga acaccaatat tacagtttgt 540

gctttccatt atgagtccca aaattcaacc cttccgatag ggctgggcct gaccaaaaat 600

atactgggtt tcctgtttcc ttttctgatc attcttacaa gttatactct tatttggaag 660

gccctaaaga aggcttatga aattcagaag aacaaaccaa gaaatgatga tatttttaag 720

ataattatgg cagcaattgt gcttttcttt ttcttttcct ggattcccca ccaaatattc 780

acttttctgg atgtattgat tcaactaggc atcatacgtg actgtagaat tgcagatatt 840

gtggacacgg ccatgcctat caccatttgt atagcttatt ttaacaattg cctgaatcct 900

ctttttatg gctttctggg gaaaaaattt aaaagatatt ttctccagct tctaaaatat 960

attcccccaa aagccaaatc ccactcaaac ctttcaacaa aaatgagcac gctttcctac 1020

cgcccctcag ataatgtaag ctcatccacc aagaagcctg caccatgttt tgaggttgag 1080

tga 1083

<210> 106
<211> 360
<212> PRT
<213> Homo sapiens

<400> 106

Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp
1 5 10 15

Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro
20 25 30

Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu
35 40 45

```
Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser
    50                  55                  60

Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr
65                  70                  75                  80

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe
                85                  90                  95

Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu
            100                 105                 110

Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu
        115                 120                 125

Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val
    130                 135                 140

Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser
145                 150                 155                 160

Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn
                165                 170                 175

Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro
            180                 185                 190

Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe
        195                 200                 205

Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys
    210                 215                 220

Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys
225                 230                 235                 240

Ile Ile Met Ala Ala Ile Val Leu Phe Phe Phe Phe Ser Trp Ile Pro
                245                 250                 255

His Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile
            260                 265                 270

Arg Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr
        275                 280                 285

Ile Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly
    290                 295                 300

Phe Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr
305                 310                 315                 320

Ile Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser
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325 330 335

Thr Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys
340 345 350

Pro Ala Pro Cys Phe Glu Val Glu
355 360

<210> 107
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 107
cccaagcttc cccaggtgta tttgat 26

<210> 108
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 108
aagcacaatt gctgcataat tatcttaaaa atatcatc 38

<210> 109
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 109
aagataatta tggcagcaat tgtgcttttc tttttcttt 39

<210> 110
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 110
gttggatcca cataatgcat tttctc 26

<210> 111
<211> 1344
<212> DNA
<213> Homo sapiens

<400> 111
atggagctgc taaagctgaa ccggagcgtg cagggaaccg gacccgggcc gggggcttcc 60

ctgtgccgcc cgggggcgcc tctcctcaac agcagcagtg tgggcaacct cagctgcgag 120

ccccctcgca ttcgcggagc cgggacacga gaattggagc tggccattag aatcactctt 180

tacgcagtga tcttcctgat gagcgttgga ggaaatatgc tcatcatcgt ggtcctggga 240

ctgagccgcc gcctgaggac tgtcaccaat gccttcctcc tctcactggc agtcagcgac 300

ctcctgctgg ctgtggcttg catgcccttc accctcctgc ccaatctcat gggcacattc 360

atctttggca ccgtcatctg caaggcggtt tcctacctca tgggggtgtc tgtgagtgtg 420

tccacgctaa gcctcgtggc catcgcactg gagcgatata gcgccatctg ccgaccactg 480

caggcacgag tgtggcagac gcgctcccac gcggctcgcg tgattgtagc cacgtggctg 540

ctgtccggac tactcatggt gccctacccc gtgtacactg tcgtgcaacc agtggggcct 600

cgtgtgctgc agtgcgtgca tcgctggccc agtgcgcggg tccgccagac ctggtccgta 660

ctgctgcttc tgctcttgtt cttcatccca ggtgtggtta tggccgtggc ctacgggctt 720

atctctcgcg agctctactt agggcttcgc tttgacggcg acagtgacag cgacagccaa 780

agcagggtcc gaaaccaagg cgggctgcca ggggctgttc accagaacgg gcgttgccgg 840

cctgagactg gcgcggttgg caaagacagc gatggctgct acgtgcaact tccacgttcc 900

cggcctgccc tggagctgac ggcgctgacg gctcctgggc cgggatccgg ctcccggccc 960

acccaggcca agctgctggc taagaagcgc gtgaaacgaa tgttgctggt gatcgttgtg 1020

ctttttttttc tgtgttggtt gccagtttat agtgccaaca cgtggcgcgc ctttgatggc 1080

ccgggtgcac accgagcact ctcgggtgct cctatctcct tcattcactt gctgagctac 1140

gcctcggcct gtgtcaaccc cctggtctac tgcttcatgc accgtcgctt tcgccaggcc 1200

tgcctggaaa cttgcgctcg ctgctgcccc cggcctccac gagctcgccc cagggctctt 1260

cccgatgagg accctcccac tccctccatt gcttcgctgt ccaggcttag ctacaccacc 1320

atcagcacac tgggccctgg ctga 1344

<210> 112
<211> 447
<212> PRT
<213> Homo sapiens

<400> 112

Met Glu Leu Leu Lys Leu Asn Arg Ser Val Gln Gly Thr Gly Pro Gly
1 5 10 15

Pro Gly Ala Ser Leu Cys Arg Pro Gly Ala Pro Leu Leu Asn Ser Ser
20 25 30

Ser Val Gly Asn Leu Ser Cys Glu Pro Pro Arg Ile Arg Gly Ala Gly
35 40 45

Thr Arg Glu Leu Glu Leu Ala Ile Arg Ile Thr Leu Tyr Ala Val Ile
50 55 60

Phe Leu Met Ser Val Gly Gly Asn Met Leu Ile Ile Val Val Leu Gly
65 70 75 80

Leu Ser Arg Arg Leu Arg Thr Val Thr Asn Ala Phe Leu Leu Ser Leu

```
                85                  90                  95

Ala Val Ser Asp Leu Leu Leu Ala Val Ala Cys Met Pro Phe Thr Leu
            100                 105                 110

Leu Pro Asn Leu Met Gly Thr Phe Ile Phe Gly Thr Val Ile Cys Lys
        115                 120                 125

Ala Val Ser Tyr Leu Met Gly Val Ser Val Ser Val Ser Thr Leu Ser
    130                 135                 140

Leu Val Ala Ile Ala Leu Glu Arg Tyr Ser Ala Ile Cys Arg Pro Leu
145                 150                 155                 160

Gln Ala Arg Val Trp Gln Thr Arg Ser His Ala Ala Arg Val Ile Val
                165                 170                 175

Ala Thr Trp Leu Leu Ser Gly Leu Leu Met Val Pro Tyr Pro Val Tyr
            180                 185                 190

Thr Val Val Gln Pro Val Gly Pro Arg Val Leu Gln Cys Val His Arg
        195                 200                 205

Trp Pro Ser Ala Arg Val Arg Gln Thr Trp Ser Val Leu Leu Leu Leu
    210                 215                 220

Leu Leu Phe Phe Ile Pro Gly Val Val Met Ala Val Ala Tyr Gly Leu
225                 230                 235                 240

Ile Ser Arg Glu Leu Tyr Leu Gly Leu Arg Phe Asp Gly Asp Ser Asp
                245                 250                 255

Ser Asp Ser Gln Ser Arg Val Arg Asn Gln Gly Gly Leu Pro Gly Ala
            260                 265                 270

Val His Gln Asn Gly Arg Cys Arg Pro Glu Thr Gly Ala Val Gly Lys
        275                 280                 285

Asp Ser Asp Gly Cys Tyr Val Gln Leu Pro Arg Ser Arg Pro Ala Leu
    290                 295                 300

Glu Leu Thr Ala Leu Thr Ala Pro Gly Pro Gly Ser Gly Ser Arg Pro
305                 310                 315                 320

Thr Gln Ala Lys Leu Leu Ala Lys Lys Arg Val Lys Arg Met Leu Leu
                325                 330                 335

Val Ile Val Val Leu Phe Phe Leu Cys Trp Leu Pro Val Tyr Ser Ala
            340                 345                 350

Asn Thr Trp Arg Ala Phe Asp Gly Pro Gly Ala His Arg Ala Leu Ser
        355                 360                 365
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Val Ala Pro Ile Ser Phe Ile His Leu Leu Ser Tyr Ala Ser Ala Cys
370 375 380

Val Asn Pro Leu Val Tyr Cys Phe Met His Arg Arg Phe Arg Gln Ala
385 390 395 400

Cys Leu Glu Thr Cys Ala Arg Cys Cys Pro Arg Pro Pro Arg Ala Arg
405 410 415

Pro Arg Ala Leu Pro Asp Glu Asp Pro Pro Thr Pro Ser Ile Ala Ser
420 425 430

Leu Ser Arg Leu Ser Tyr Thr Thr Ile Ser Thr Leu Gly Pro Gly
435 440 445

<210> 113
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 113
cagcagcatg cgcttcacgc gcttcttagc ccag 34

<210> 114
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 114
agaagcgcgt gaagcgcatg ctgctggtga tcgtt 35

<210> 115
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 115
atggagaaaa gaatcaaaag aatgttctat ata 33

<210> 116
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 116
tatatagaac attcttttga ttcttttctc cat 33

<210> 117

<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 117
cgctctctgg ccttgaagcg cacgctcagc 30

<210> 118
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 118
gctgagcgtg cgcttcaagg ccagagagcg 30

<210> 119
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 119
cccaggaaaa aggtgaaagt caaagttttc 30

<210> 120
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 120
gaaaactttg actttcacct ttttcctggg 30

<210> 121
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 121
ggggcgcggg tgaaacggct ggtgagc 27

<210> 122
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 122
gctcaccagc cgtttcaccc gcgcccc 27

<210> 123
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 123
cccttgaaa agcctaagaa cttggtcatc 30

<210> 124
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 124
gatgaccaag ttcttaggct tttcaagggg 30

<210> 125
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 125
gatctctaga atgaacagca catgtattga ag 32

<210> 126
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 126
ctagggtacc cgctcaagga cctctaattc catag 35

<210> 127
<211> 1296
<212> DNA
<213> Homo sapiens

<400> 127
atgcaggcgc ttaacattac cccggagcag ttctctcggc tgctgcggga ccacaacctg 60

acgcgggagc agttcatcgc tctgtaccgg ctgcgaccgc tcgtctacac cccagagctg 120

ccgggacgcg ccaagctggc cctcgtgctc accggcgtgc tcatcttcgc cctggcgctc 180

tttggcaatg ctctggtgtt ctacgtggtg acccgcagca aggccatgcg caccgtcacc 240

aacatcttta tctgctcctt ggcgctcagt gacctgctca tcaccttctt ctgcattccc 300

gtcaccatgc tccagaacat ttccgacaac tggctggggg gtgctttcat ttgcaagatg 360

gtgccatttg tccagtctac cgctgttgtg acagaaatgc tcactatgac ctgcattgct 420

gtggaaaggc accagggact tgtgcatcct tttaaaatga agtggcaata caccaaccga 480

agggctttca caatgctagg tgtggtctgg ctggtggcag tcatcgtagg atcacccatg 540

tggcacgtgc aacaacttga gatcaaatat gacttcctat atgaaaagga acacatctgc 600

tgcttagaag agtggaccag ccctgtgcac cagaagatct acaccacctt catccttgtc 660

atcctcttcc tcctgcctct tatggtgatg cttattctgt acagtaaaat tggttatgaa 720

ctttggataa agaaaagagt tggggatggt tcagtgcttc gaactattca tggaaaagaa 780

atgtccaaaa tagccaggaa gaagaaacga gctaagatta tgatggtgac agtggtggct 840

ctctttgctg tgtgctgggc accattccat gttgtccata tgatgattga atacagtaat 900

tttgaaaagg aatatgatga tgtcacaatc aagatgattt ttgctatcgt gcaaattatt 960

ggattttcca actccatctg taatcccatt gtctatgcat ttatgaatga aaacttcaaa 1020

aaaaatgttt tgtctgcagt ttgttattgc atagtaaata aaaccttctc tccagcacaa 1080

aggcatggaa attcaggaat tacaatgatg cggaagaaag caaagttttc cctcagagag 1140

aatccagtgg aggaaaccaa aggagaagca ttcagtgatg gcaacattga agtcaaattg 1200

tgtgaacaga cagaggagaa gaaaaagctc aaacgacatc ttgctctctt taggtctgaa 1260

ctggctgaga attctccttt agacagtggg cattaa 1296

<210> 128
<211> 431
<212> PRT
<213> Homo sapiens

<400> 128

Met Gln Ala Leu Asn Ile Thr Pro Glu Gln Phe Ser Arg Leu Leu Arg
1 5 10 15

Asp His Asn Leu Thr Arg Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg
20 25 30

Pro Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu
35 40 45

Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala
50 55 60

Leu Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr
65 70 75 80

Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe
85 90 95

Phe Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Asn Trp Leu
100 105 110

Gly Gly Ala Phe Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala
115 120 125

Val Val Thr Glu Met Leu Thr Met Thr Cys Ile Ala Val Glu Arg His

```
    130                 135                 140

Gln Gly Leu Val His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg
145                 150                 155                 160

Arg Ala Phe Thr Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val
                165                 170                 175

Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe
            180                 185                 190

Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro
        195                 200                 205

Val His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu
    210                 215                 220

Leu Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile Gly Tyr Glu
225                 230                 235                 240

Leu Trp Ile Lys Lys Arg Val Gly Asp Gly Ser Val Leu Arg Thr Ile
                245                 250                 255

His Gly Lys Glu Met Ser Lys Ile Ala Arg Lys Lys Lys Arg Ala Lys
            260                 265                 270

Ile Met Met Val Thr Val Val Ala Leu Phe Ala Val Cys Trp Ala Pro
        275                 280                 285

Phe His Val Val His Met Met Ile Glu Tyr Ser Asn Phe Glu Lys Glu
    290                 295                 300

Tyr Asp Asp Val Thr Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile
305                 310                 315                 320

Gly Phe Ser Asn Ser Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn
                325                 330                 335

Glu Asn Phe Lys Lys Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val
            340                 345                 350

Asn Lys Thr Phe Ser Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr
        355                 360                 365

Met Met Arg Lys Lys Ala Lys Phe Ser Leu Arg Glu Asn Pro Val Glu
    370                 375                 380

Glu Thr Lys Gly Glu Ala Phe Ser Asp Gly Asn Ile Glu Val Lys Leu
385                 390                 395                 400

Cys Glu Gln Thr Glu Glu Lys Lys Lys Leu Lys Arg His Leu Ala Leu
                405                 410                 415
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Phe Arg Ser Glu Leu Ala Glu Asn Ser Pro Leu Asp Ser Gly His
420 425 430

<210> 129
<211> 2040
<212> DNA
<213> Homo sapiens

<400> 129
atgggcagcc cctggaacgg cagcgacggc cccgaggggg cgcgggagcc gccgtggccc 60

gcgctgccgc cttgcgacga gcgccgctgc tcgcccttc ccctgggggc gctggtgccg 120

gtgaccgctg tgtgcctgtg cctgttcgtc gtcggggtga gcggcaacgt ggtgaccgtg 180

atgctgatcg ggcgctaccg ggacatgcgg accaccacca acttgtacct gggcagcatg 240

gccgtgtccg acctactcat cctgctcggg ctgccgttcg acctgtaccg cctctggcgc 300

tcgcggccct gggtgttcgg gccgctgctc tgccgcctgt ccctctacgt gggcgagggc 360

tgcacctacg ccacgctgct gcacatgacc gcgctcagcg tcgagcgcta cctggccatc 420

tgccgcccgc tccgcgcccg cgtcttggtc acccggcgcc gcgtccgcgc gctcatcgct 480

gtgctctggg ccgtggcgct gctctctgcc ggtcccttct tgttcctggt gggcgtcgag 540

caggaccccg gcatctccgt agtcccgggc ctcaatggca ccgcgcggat cgcctcctcg 600

cctctcgcct cgtcgccgcc tctctggctc tcgcgggcgc caccgccgtc cccgccgtcg 660

gggcccgaga ccgcggaggc cgcggcgctg ttcagccgcg aatgccggcc gagccccgcg 720

cagctgggcg cgctgcgtgt catgctgtgg gtcaccaccg cctacttctt cctgcccttt 780

ctgtgcctca gcatcctcta cgggctcatc gggcgggagc tgtggagcag ccggcggccg 840

ctgcgaggcc cggccgcctc ggggcgggag agaggccacc ggcagaccaa acgcgtcctg 900

cgtaagtgga gccgccgtgg ttccaaagac gcctgcctgc agtccgcccc gccggggacc 960

gcgcaaacgc tgggtcccct tcccctgctc gcccagctct gggcgccgct tccagctccc 1020

tttcctattt cgattccagc ctccacccgc cggtacttcc catcccccga gaaaaccatg 1080

tcctgtcccc caggagctct gggggacccc agggcgcttt gagggtggga tccccggatc 1140

cgattcagta accagcagtg cttttccaga gcctctgaga ccagaaagga gagttggtaa 1200

ttcttaatcc aaccacctgt tagatgccac aaatgaggag tcctcacagt gctcttgaga 1260

agacgaggga gatttcatta agctaaaatt ttttatttaa tgttaagtga tgctgaaggc 1320

taaagtaaac cttgctcgta tcaaaaagta aagattgtgc agacctgttg tagaattctt 1380

ttcaacagag aacagaaaac ttgtctccga agtgggtttg tggaaggaag cctgccaagg 1440

cggcttgttc agagaaattg ctccttctgg tttatgtcca gccttgataa cacatatggg 1500

agcctactat gcagttttaa agcaagtatc catgcagcct gcagcctggt catttttttct 1560

ggggtgagga tctgcctagg tagaagtttt ctctaattta ttttgctgtt acttgttatt 1620

gcagatggtt ccttgtcggg gtgggggggtt tatttgcttc ccaatgcttt tgttaatccc 1680

ggtgctgtgt cttatgttgc agtggtggtg gttctggcat ttataatttg ctggttgccc 1740

ttccacgttg gcagaatcat ttacataaac acggaagatt cgcggatgat gtacttctct 1800

cagtacttta acatcgtcgc tctgcaactt ttctatctga gcgcatctat caacccaatc 1860

ctctacaacc tcatttcaaa gaagtacaga gcggcggcct ttaaactgct gctcgcaagg 1920

aagtccaggc cgagaggctt ccacagaagc agggacactg cgggggaagt tgcaggggac 1980

actggaggag acacggtggg ctacaccgag acaagcgcta acgtgaagac gatgggataa 2040

<210> 130
<211> 412
<212> PRT
<213> Homo sapiens

<400> 130

Met Gly Ser Pro Trp Asn Gly Ser Asp Gly Pro Glu Gly Ala Arg Glu
1 5 10 15

Pro Pro Trp Pro Ala Leu Pro Pro Cys Asp Glu Arg Arg Cys Ser Pro
20 25 30

Phe Pro Leu Gly Ala Leu Val Pro Val Thr Ala Val Cys Leu Cys Leu
35 40 45

Phe Val Val Gly Val Ser Gly Asn Val Val Thr Val Met Leu Ile Gly
50 55 60

Arg Tyr Arg Asp Met Arg Thr Thr Thr Asn Leu Tyr Leu Gly Ser Met
65 70 75 80

Ala Val Ser Asp Leu Leu Ile Leu Leu Gly Leu Pro Phe Asp Leu Tyr
85 90 95

Arg Leu Trp Arg Ser Arg Pro Trp Val Phe Gly Pro Leu Leu Cys Arg
100 105 110

Leu Ser Leu Tyr Val Gly Glu Gly Cys Thr Tyr Ala Thr Leu Leu His
115 120 125

Met Thr Ala Leu Ser Val Glu Arg Tyr Leu Ala Ile Cys Arg Pro Leu
130 135 140

Arg Ala Arg Val Leu Val Thr Arg Arg Arg Val Arg Ala Leu Ile Ala
145 150 155 160

Val Leu Trp Ala Val Ala Leu Leu Ser Ala Gly Pro Phe Leu Phe Leu
165 170 175

Val Gly Val Glu Gln Asp Pro Gly Ile Ser Val Val Pro Gly Leu Asn
180 185 190

Gly Thr Ala Arg Ile Ala Ser Ser Pro Leu Ala Ser Ser Pro Pro Leu
195 200 205

Trp Leu Ser Arg Ala Pro Pro Pro Ser Pro Pro Ser Gly Pro Glu Thr

210 215 220

Ala Glu Ala Ala Ala Leu Phe Ser Arg Glu Cys Arg Pro Ser Pro Ala
225 230 235 240

Gln Leu Gly Ala Leu Arg Val Met Leu Trp Val Thr Thr Ala Tyr Phe
245 250 255

Phe Leu Pro Phe Leu Cys Leu Ser Ile Leu Tyr Gly Leu Ile Gly Arg
260 265 270

Glu Leu Trp Ser Ser Arg Arg Pro Leu Arg Gly Pro Ala Ala Ser Gly
275 280 285

Arg Glu Arg Gly His Arg Gln Thr Lys Arg Val Leu Leu Val Val Val
290 295 300

Leu Ala Phe Ile Ile Cys Trp Leu Pro Phe His Val Gly Arg Ile Ile
305 310 315 320

Tyr Ile Asn Thr Glu Asp Ser Arg Met Met Tyr Phe Ser Gln Tyr Phe
325 330 335

Asn Ile Val Ala Leu Gln Leu Phe Tyr Leu Ser Ala Ser Ile Asn Pro
340 345 350

Ile Leu Tyr Asn Leu Ile Ser Lys Lys Tyr Arg Ala Ala Ala Phe Lys
355 360 365

Leu Leu Leu Ala Arg Lys Ser Arg Pro Arg Gly Phe His Arg Ser Arg
370 375 380

Asp Thr Ala Gly Glu Val Ala Gly Asp Thr Gly Gly Asp Thr Val Gly
385 390 395 400

Tyr Thr Glu Thr Ser Ala Asn Val Lys Thr Met Gly
405 410

<210> 131
<211> 1344
<212> DNA
<213> Homo sapiens

<400> 131
atggagctgc taaagctgaa ccggagcgtg cagggaaccg gacccgggcc gggggcttcc 60

ctgtgccgcc cgggggcgcc tctcctcaac agcagcagtg tgggcaacct cagctgcgag 120

ccccctcgca ttcgcggagc cgggacacga gaattggagc tggccattag aatcactctt 180

tacgcagtga tcttcctgat gagcgttgga ggaaatatgc tcatcatcgt ggtcctggga 240

ctgagccgcc gcctgaggac tgtcaccaat gccttcctcc tctcactggc agtcagcgac 300

ctcctgctgg ctgtggcttg catgcccttc accctcctgc ccaatctcat gggcacattc 360

atctttggca ccgtcatctg caaggcggtt tcctacctca tgggggtgtc tgtgagtgtg 420

tccacgctaa gcctcgtggc catcgcactg gagcgatata gcgccatctg ccgaccactg 480

caggcacgag tgtggcagac gcgctcccac gcggctcgcg tgattgtagc cacgtggctg 540

ctgtccggac tactcatggt gccctacccc gtgtacactg tcgtgcaacc agtggggcct 600

cgtgtgctgc agtgcgtgca tcgctggccc agtgcgcggg tccgccagac ctggtccgta 660

ctgctgcttc tgctcttgtt cttcatccca ggtgtggtta tggccgtggc ctacgggctt 720

atctctcgcg agctctactt agggcttcgc tttgacggcg acagtgacag cgacagccaa 780

agcagggtcc gaaaccaagg cgggctgcca ggggctgttc accagaacgg gcgttgccgg 840

cctgagactg gcgcggttgg caaagacagc gatggctgct acgtgcaact tccacgttcc 900

cggcctgccc tggagctgac ggcgctgacg gctcctgggc cgggatccgg ctcccggccc 960

acccaggcca agctgctggc taagaagcgc gtgaaacgaa tgttgctggt gatcgttgtg 1020

ctttttttc tgtgttggtt gccagtttat agtgccaaca cgtggcgcgc ctttgatggc 1080

ccgggtgcac accgagcact ctcgggtgct cctatctcct tcattcactt gctgagctac 1140

gcctcggcct gtgtcaaccc cctggtctac tgcttcatgc accgtcgctt tcgccaggcc 1200

tgcctggaaa cttgcgctcg ctgctgcccc cggcctccac gagctcgccc cagggctctt 1260

cccgatgagg accctcccac tccctccatt gcttcgctgt ccaggcttag ctacaccacc 1320

atcagcacac tgggccctgg ctga 1344

<210> 132
<211> 447
<212> PRT
<213> Homo sapiens

<400> 132

Met Glu Leu Leu Lys Leu Asn Arg Ser Val Gln Gly Thr Gly Pro Gly
1 5 10 15

Pro Gly Ala Ser Leu Cys Arg Pro Gly Ala Pro Leu Leu Asn Ser Ser
20 25 30

Ser Val Gly Asn Leu Ser Cys Glu Pro Pro Arg Ile Arg Gly Ala Gly
35 40 45

Thr Arg Glu Leu Glu Leu Ala Ile Arg Ile Thr Leu Tyr Ala Val Ile
50 55 60

Phe Leu Met Ser Val Gly Gly Asn Met Leu Ile Ile Val Val Leu Gly
65 70 75 80

Leu Ser Arg Arg Leu Arg Thr Val Thr Asn Ala Phe Leu Leu Ser Leu
85 90 95

Ala Val Ser Asp Leu Leu Leu Ala Val Ala Cys Met Pro Phe Thr Leu
100 105 110

Leu Pro Asn Leu Met Gly Thr Phe Ile Phe Gly Thr Val Ile Cys Lys

```
        115                 120                 125

Ala Val Ser Tyr Leu Met Gly Val Ser Val Ser Val Ser Thr Leu Ser
    130                 135                 140

Leu Val Ala Ile Ala Leu Glu Arg Tyr Ser Ala Ile Cys Arg Pro Leu
145                 150                 155                 160

Gln Ala Arg Val Trp Gln Thr Arg Ser His Ala Ala Arg Val Ile Val
                165                 170                 175

Ala Thr Trp Leu Leu Ser Gly Leu Leu Met Val Pro Tyr Pro Val Tyr
            180                 185                 190

Thr Val Val Gln Pro Val Gly Pro Arg Val Leu Gln Cys Val His Arg
        195                 200                 205

Trp Pro Ser Ala Arg Val Arg Gln Thr Trp Ser Val Leu Leu Leu Leu
    210                 215                 220

Leu Leu Phe Phe Ile Pro Gly Val Val Met Ala Val Ala Tyr Gly Leu
225                 230                 235                 240

Ile Ser Arg Glu Leu Tyr Leu Gly Leu Arg Phe Asp Gly Asp Ser Asp
                245                 250                 255

Ser Asp Ser Gln Ser Arg Val Arg Asn Gln Gly Gly Leu Pro Gly Ala
            260                 265                 270

Val His Gln Asn Gly Arg Cys Arg Pro Glu Thr Gly Ala Val Gly Lys
        275                 280                 285

Asp Ser Asp Gly Cys Tyr Val Gln Leu Pro Arg Ser Arg Pro Ala Leu
    290                 295                 300

Glu Leu Thr Ala Leu Thr Ala Pro Gly Pro Gly Ser Gly Ser Arg Pro
305                 310                 315                 320

Thr Gln Ala Lys Leu Leu Ala Lys Lys Arg Val Lys Arg Met Leu Leu
                325                 330                 335

Val Ile Val Val Leu Phe Phe Leu Cys Trp Leu Pro Val Tyr Ser Ala
            340                 345                 350

Asn Thr Trp Arg Ala Phe Asp Gly Pro Gly Ala His Arg Ala Leu Ser
        355                 360                 365

Val Ala Pro Ile Ser Phe Ile His Leu Leu Ser Tyr Ala Ser Ala Cys
    370                 375                 380

Val Asn Pro Leu Val Tyr Cys Phe Met His Arg Arg Phe Arg Gln Ala
385                 390                 395                 400
```

Cys Leu Glu Thr Cys Ala Arg Cys Cys Pro Arg Pro Pro Arg Ala Arg
405 410 415

Pro Arg Ala Leu Pro Asp Glu Asp Pro Pro Thr Pro Ser Ile Ala Ser
420 425 430

Leu Ser Arg Leu Ser Tyr Thr Thr Ile Ser Thr Leu Gly Pro Gly
435 440 445

<210> 133
<211> 1014
<212> DNA
<213> Homo sapiens

<400> 133
atgaacagca catgtattga agaacagcat gacctggatc actatttgtt tcccattgtt 60

tacatctttg tgattatagt cagcattcca gccaatattg gatctctgtg tgtgtctttc 120

ctgcaagcaa agaaggaaag tgaactagga atttacctct tcagtttgtc actatcagat 180

ttactctatg cattaactct ccctttatgg attgattata cttggaataa agacaactgg 240

actttctctc ctgccttgtg caaagggagt gcttttctca tgtacatgaa tttttacagc 300

agcacagcat tcctcacctg cattgccgtt gatcggtatt tggctgttgt ctacccttg 360

aagtttttt tcctaaggac aagaagattt gcactcatgg tcagcctgtc catctggata 420

ttggaaacca tcttcaatgc tgtcatgttg tgggaagatg aaacagttgt tgaatattgc 480

gatgccgaaa agtctaattt tactttatgc tatgacaaat acccttaga gaaatggcaa 540

atcaacctca acttgttcag gacgtgtaca ggctatgcaa tacctttggt caccatcctg 600

atctgtaacc ggaaagtcta ccaagctgtg cggcacaata aagccacgga aaacaaggaa 660

aagaagagaa tcaaaaaact acttgtcagc atcacagtta cttttgtctt atgctttact 720

ccctttcatg tgatgttgct gattcgctgc attttagagc atgctgtgaa cttcgaagac 780

cacagcaatt ctgggaagcg aacttacaca atgtatagaa tcacggttgc attaacaagt 840

ttaaattgtg ttgctgatcc aattctgtac tgttttgtta ccgaaacagg aagatatgat 900

atgtggaata tattaaaatt ctgcactggg aggtgtaata catcacaaag acaaagaaaa 960

cgcatacttt ctgtgtctac aaaagatact atggaattag aggtccttga gtag 1014

<210> 134
<211> 337
<212> PRT
<213> Homo sapiens

<400> 134

Met Asn Ser Thr Cys Ile Glu Glu Gln His Asp Leu Asp His Tyr Leu
1 5 10 15

Phe Pro Ile Val Tyr Ile Phe Val Ile Ile Val Ser Ile Pro Ala Asn
20 25 30

Ile Gly Ser Leu Cys Val Ser Phe Leu Gln Ala Lys Lys Glu Ser Glu

```
        35                  40                  45

Leu Gly Ile Tyr Leu Phe Ser Leu Ser Leu Ser Asp Leu Leu Tyr Ala
    50                  55                  60

Leu Thr Leu Pro Leu Trp Ile Asp Tyr Thr Trp Asn Lys Asp Asn Trp
65                  70                  75                  80

Thr Phe Ser Pro Ala Leu Cys Lys Gly Ser Ala Phe Leu Met Tyr Met
                85                  90                  95

Asn Phe Tyr Ser Ser Thr Ala Phe Leu Thr Cys Ile Ala Val Asp Arg
            100                 105                 110

Tyr Leu Ala Val Val Tyr Pro Leu Lys Phe Phe Phe Leu Arg Thr Arg
        115                 120                 125

Arg Phe Ala Leu Met Val Ser Leu Ser Ile Trp Ile Leu Glu Thr Ile
    130                 135                 140

Phe Asn Ala Val Met Leu Trp Glu Asp Glu Thr Val Val Glu Tyr Cys
145                 150                 155                 160

Asp Ala Glu Lys Ser Asn Phe Thr Leu Cys Tyr Asp Lys Tyr Pro Leu
                165                 170                 175

Glu Lys Trp Gln Ile Asn Leu Asn Leu Phe Arg Thr Cys Thr Gly Tyr
            180                 185                 190

Ala Ile Pro Leu Val Thr Ile Leu Ile Cys Asn Arg Lys Val Tyr Gln
        195                 200                 205

Ala Val Arg His Asn Lys Ala Thr Glu Asn Lys Glu Lys Lys Arg Ile
    210                 215                 220

Lys Lys Leu Leu Val Ser Ile Thr Val Thr Phe Val Leu Cys Phe Thr
225                 230                 235                 240

Pro Phe His Val Met Leu Leu Ile Arg Cys Ile Leu Glu His Ala Val
                245                 250                 255

Asn Phe Glu Asp His Ser Asn Ser Gly Lys Arg Thr Tyr Thr Met Tyr
            260                 265                 270

Arg Ile Thr Val Ala Leu Thr Ser Leu Asn Cys Val Ala Asp Pro Ile
        275                 280                 285

Leu Tyr Cys Phe Val Thr Glu Thr Gly Arg Tyr Asp Met Trp Asn Ile
    290                 295                 300

Leu Lys Phe Cys Thr Gly Arg Cys Asn Thr Ser Gln Arg Gln Arg Lys
305                 310                 315                 320
```

Arg Ile Leu Ser Val Ser Thr Lys Asp Thr Met Glu Leu Glu Val Leu
325 330 335

Glu

<210> 135
<211> 999
<212> DNA
<213> Homo sapiens

<400> 135
atggtgaact ccacccaccg tgggatgcac acttctctgc acctctggaa ccgcagcagt 60

tacagactgc acagcaatgc cagtgagtcc cttggaaaag gctactctga tggagggtgc 120

tacgagcaac tttttgtctc tcctgaggtg tttgtgactc tgggtgtcat cagcttgttg 180

gagaatatct tagtgattgt ggcaatagcc aagaacaaga atctgcattc acccatgtac 240

tttttcatct gcagcttggc tgtggctgat atgctggtga gcgtttcaaa tggatcagaa 300

accattatca tcaccctatt aaacagtaca gatacggatg cacagagttt cacagtgaat 360

attgataatg tcattgactc ggtgatctgt agctccttgc ttgcatccat ttgcagcctg 420

ctttcaattg cagtggacag gtactttact atcttctatg ctctccagta ccataacatt 480

atgacagtta agcgggttgg gatcagcata agttgtatct gggcagcttg cacggtttca 540

ggcattttgt tcatcattta ctcagatagt agtgctgtca tcatctgcct catcaccatg 600

ttcttcacca tgctggctct catggcttct ctctatgtcc acatgttcct gatggccagg 660

cttcacatta agaggattgc tgtcctcccc ggcactggtg ccatccgcca aggtgccaat 720

atgaagggaa aaattacctt gaccatcctg attggcgtct ttgttgtctg ctgggcccca 780

ttcttcctcc acttaatatt ctacatctct tgtcctcaga atccatattg tgtgtgcttc 840

atgtctcact ttaacttgta tctcatactg atcatgtgta attcaatcat cgatcctctg 900

atttatgcac tccggagtca agaactgagg aaaaccttca aagagatcat ctgttgctat 960

cccctgggag gcctttgtga cttgtctagc agatattaa 999

<210> 136
<211> 332
<212> PRT
<213> Homo sapiens

<400> 136

Met Val Asn Ser Thr His Arg Gly Met His Thr Ser Leu His Leu Trp
1 5 10 15

Asn Arg Ser Ser Tyr Arg Leu His Ser Asn Ala Ser Glu Ser Leu Gly
20 25 30

Lys Gly Tyr Ser Asp Gly Gly Cys Tyr Glu Gln Leu Phe Val Ser Pro
35 40 45

Glu Val Phe Val Thr Leu Gly Val Ile Ser Leu Leu Glu Asn Ile Leu

```
    50                  55                  60

Val Ile Val Ala Ile Ala Lys Asn Lys Asn Leu His Ser Pro Met Tyr
65                  70                  75                  80

Phe Phe Ile Cys Ser Leu Ala Val Ala Asp Met Leu Val Ser Val Ser
                85                  90                  95

Asn Gly Ser Glu Thr Ile Ile Ile Thr Leu Leu Asn Ser Thr Asp Thr
            100                 105                 110

Asp Ala Gln Ser Phe Thr Val Asn Ile Asp Asn Val Ile Asp Ser Val
        115                 120                 125

Ile Cys Ser Ser Leu Leu Ala Ser Ile Cys Ser Leu Leu Ser Ile Ala
    130                 135                 140

Val Asp Arg Tyr Phe Thr Ile Phe Tyr Ala Leu Gln Tyr His Asn Ile
145                 150                 155                 160

Met Thr Val Lys Arg Val Gly Ile Ser Ile Ser Cys Ile Trp Ala Ala
                165                 170                 175

Cys Thr Val Ser Gly Ile Leu Phe Ile Ile Tyr Ser Asp Ser Ser Ala
            180                 185                 190

Val Ile Ile Cys Leu Ile Thr Met Phe Phe Thr Met Leu Ala Leu Met
        195                 200                 205

Ala Ser Leu Tyr Val His Met Phe Leu Met Ala Arg Leu His Ile Lys
    210                 215                 220

Arg Ile Ala Val Leu Pro Gly Thr Gly Ala Ile Arg Gln Gly Ala Asn
225                 230                 235                 240

Met Lys Gly Lys Ile Thr Leu Thr Ile Leu Ile Gly Val Phe Val Val
                245                 250                 255

Cys Trp Ala Pro Phe Phe Leu His Leu Ile Phe Tyr Ile Ser Cys Pro
            260                 265                 270

Gln Asn Pro Tyr Cys Val Cys Phe Met Ser His Phe Asn Leu Tyr Leu
        275                 280                 285

Ile Leu Ile Met Cys Asn Ser Ile Ile Asp Pro Leu Ile Tyr Ala Leu
    290                 295                 300

Arg Ser Gln Glu Leu Arg Lys Thr Phe Lys Glu Ile Ile Cys Cys Tyr
305                 310                 315                 320

Pro Leu Gly Gly Leu Cys Asp Leu Ser Ser Arg Tyr
                325                 330
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<210> 137
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 137
gccaatatga agggaaaaat taccttgacc atc 33

<210> 138
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 138
ctccttcggt cctcctatcg ttgtcagaag t 31

<210> 139
<211> 1842
<212> DNA
<213> Homo sapiens

<400> 139
atggggccca ccctagcggt tcccaccccc tatggctgta ttggctgtaa gctaccccag 60

ccagaatacc caccggctct aatcatcttt atgttctgcg cgatggttat caccatcgtt 120

gtagacctaa tcggcaactc catggtcatt ttggctgtga cgaagaacaa gaagctccgg 180

aattctggca acatcttcgt ggtcagtctc tctgtggccg atatgctggt ggccatctac 240

ccataccctt tgatgctgca tgccatgtcc attgggggct gggatctgag ccagttacag 300

tgccagatgg tcgggttcat cacagggctg agtgtggtcg gctccatctt caacatcgtg 360

gcaatcgcta tcaaccgtta ctgctacatc tgccacagcc tccagtacga acggatcttc 420

agtgtgcgca atacctgcat ctacctggtc atcacctgga tcatgaccgt cctggctgtc 480

ctgcccaaca tgtacattgg caccatcgag tacgatcctc gcacctacac ctgcatcttc 540

aactatctga acaaccctgt cttcactgtt accatcgtct gcatccactt cgtcctccct 600

ctcctcatcg tgggtttctg ctacgtgagg atctggacca aagtgctggc ggcccgtgac 660

cctgcagggc agaatcctga caaccaactt gctgaggttc gcaattttct aaccatgttt 720

gtgatcttcc tcctctttgc agtgtgctgg tgccctatca acgtgctcac tgtcttggtg 780

gctgtcagtc cgaaggagat ggcaggcaag atccccaact ggctttatct tgcagcctac 840

ttcatagcct acttcaacag ctgcctcaac gctgtgatct acgggctcct caatgagaat 900

ttccgaagag aatactggac catcttccat gctatgcggc accctatcat attcttccct 960

ggcctcatca gtgatattcg tgagatgcag gaggcccgta ccctggcccg cgcccgtgcc 1020

catgctcgcg accaagctcg tgaacaagac cgtgcccatg cctgtcctgc tgtggaggaa 1080

accccgatga atgtccggaa tgttccatta cctggtgatg ctgcagctgg ccacccccgac 1140

cgtgcctctg gccaccctaa gccccattcc agatcctcct ctgcctatcg caaatctgcc 1200

tctacccacc acaagtctgt ctttagccac tccaaggctg cctctggtca cctcaagcct 1260

gtctctggcc actccaagcc tgcctctggt caccccaagt ctgccactgt ctaccctaag 1320

cctgcctctg tccatttcaa gggtgactct gtccatttca agggtgactc tgtccatttc 1380

aagcctgact ctgttcattt caagcctgct tccagcaacc ccaagcccat cactggccac 1440

catgtctctg ctggcagcca ctccaagtct gccttcagtg ctgccaccag ccaccctaaa 1500

cccatcaagc cagctaccag ccatgctgag cccaccactg ctgactatcc caagcctgcc 1560

actaccagcc accctaagcc cgctgctgct gacaaccctg agctctctgc ctcccattgc 1620

cccgagatcc ctgccattgc ccaccctgtg tctgacgaca gtgacctccc tgagtcggcc 1680

tctagccctg ccgctgggcc caccaagcct gctgccagcc agctggagtc tgacaccatc 1740

gctgaccttc ctgaccctac tgtagtcact accagtacca atgattacca tgatgtcgtg 1800

gttgttgatg ttgaagatga tcctgatgaa atggctgtgt ga 1842

<210> 140
<211> 613
<212> PRT
<213> Homo sapiens

<400> 140

Met Gly Pro Thr Leu Ala Val Pro Thr Pro Tyr Gly Cys Ile Gly Cys
1 5 10 15

Lys Leu Pro Gln Pro Glu Tyr Pro Pro Ala Leu Ile Ile Phe Met Phe
20 25 30

Cys Ala Met Val Ile Thr Ile Val Val Asp Leu Ile Gly Asn Ser Met
35 40 45

Val Ile Leu Ala Val Thr Lys Asn Lys Lys Leu Arg Asn Ser Gly Asn
50 55 60

Ile Phe Val Val Ser Leu Ser Val Ala Asp Met Leu Val Ala Ile Tyr
65 70 75 80

Pro Tyr Pro Leu Met Leu His Ala Met Ser Ile Gly Gly Trp Asp Leu
85 90 95

Ser Gln Leu Gln Cys Gln Met Val Gly Phe Ile Thr Gly Leu Ser Val
100 105 110

Val Gly Ser Ile Phe Asn Ile Val Ala Ile Ala Ile Asn Arg Tyr Cys
115 120 125

Tyr Ile Cys His Ser Leu Gln Tyr Glu Arg Ile Phe Ser Val Arg Asn
130 135 140

Thr Cys Ile Tyr Leu Val Ile Thr Trp Ile Met Thr Val Leu Ala Val
145 150 155 160

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Leu Pro Asn Met Tyr Ile Gly Thr Ile Glu Tyr Asp Pro Arg Thr Tyr
                165                 170                 175

Thr Cys Ile Phe Asn Tyr Leu Asn Asn Pro Val Phe Thr Val Thr Ile
            180                 185                 190

Val Cys Ile His Phe Val Leu Pro Leu Leu Ile Val Gly Phe Cys Tyr
        195                 200                 205

Val Arg Ile Trp Thr Lys Val Leu Ala Ala Arg Asp Pro Ala Gly Gln
    210                 215                 220

Asn Pro Asp Asn Gln Leu Ala Glu Val Arg Asn Phe Leu Thr Met Phe
225                 230                 235                 240

Val Ile Phe Leu Leu Phe Ala Val Cys Trp Cys Pro Ile Asn Val Leu
                245                 250                 255

Thr Val Leu Val Ala Val Ser Pro Lys Glu Met Ala Gly Lys Ile Pro
            260                 265                 270

Asn Trp Leu Tyr Leu Ala Ala Tyr Phe Ile Ala Tyr Phe Asn Ser Cys
        275                 280                 285

Leu Asn Ala Val Ile Tyr Gly Leu Leu Asn Glu Asn Phe Arg Arg Glu
    290                 295                 300

Tyr Trp Thr Ile Phe His Ala Met Arg His Pro Ile Ile Phe Phe Pro
305                 310                 315                 320

Gly Leu Ile Ser Asp Ile Arg Glu Met Gln Glu Ala Arg Thr Leu Ala
                325                 330                 335

Arg Ala Arg Ala His Ala Arg Asp Gln Ala Arg Glu Gln Asp Arg Ala
            340                 345                 350

His Ala Cys Pro Ala Val Glu Glu Thr Pro Met Asn Val Arg Asn Val
        355                 360                 365

Pro Leu Pro Gly Asp Ala Ala Ala Gly His Pro Asp Arg Ala Ser Gly
    370                 375                 380

His Pro Lys Pro His Ser Arg Ser Ser Ser Ala Tyr Arg Lys Ser Ala
385                 390                 395                 400

Ser Thr His His Lys Ser Val Phe Ser His Ser Lys Ala Ala Ser Gly
                405                 410                 415

His Leu Lys Pro Val Ser Gly His Ser Lys Pro Ala Ser Gly His Pro
            420                 425                 430

Lys Ser Ala Thr Val Tyr Pro Lys Pro Ala Ser Val His Phe Lys Gly
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435 440 445

Asp Ser Val His Phe Lys Gly Asp Ser Val His Phe Lys Pro Asp Ser
450 455 460

Val His Phe Lys Pro Ala Ser Ser Asn Pro Lys Pro Ile Thr Gly His
465 470 475 480

His Val Ser Ala Gly Ser His Ser Lys Ser Ala Phe Ser Ala Ala Thr
485 490 495

Ser His Pro Lys Pro Ile Lys Pro Ala Thr Ser His Ala Glu Pro Thr
500 505 510

Thr Ala Asp Tyr Pro Lys Pro Ala Thr Thr Ser His Pro Lys Pro Ala
515 520 525

Ala Ala Asp Asn Pro Glu Leu Ser Ala Ser His Cys Pro Glu Ile Pro
530 535 540

Ala Ile Ala His Pro Val Ser Asp Asp Ser Asp Leu Pro Glu Ser Ala
545 550 555 560

Ser Ser Pro Ala Ala Gly Pro Thr Lys Pro Ala Ala Ser Gln Leu Glu
565 570 575

Ser Asp Thr Ile Ala Asp Leu Pro Asp Pro Thr Val Val Thr Thr Ser
580 585 590

Thr Asn Asp Tyr His Asp Val Val Val Val Asp Val Glu Asp Asp Pro
595 600 605

Asp Glu Met Ala Val
610

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<212> DNA
<213> Homo sapiens

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gtagacctaa tcggcaactc catggtcatt ttggctgtga cgaagaacaa gaagctccgg 180

aattctggca acatcttcgt ggtcagtctc tctgtggccg atatgctggt ggccatctac 240

ccataccctt tgatgctgca tgccatgtcc attgggggct gggatctgag ccagttacag 300

tgccagatgg tcgggttcat cacagggctg agtgtggtcg gctccatctt caacatcgtg 360

gcaatcgcta tcaaccgtta ctgctacatc tgccacagcc tccagtacga acggatcttc 420

agtgtgcgca atacctgcat ctacctggtc atcacctgga tcatgaccgt cctggctgtc 480

ctgcccaaca tgtacattgg caccatcgag tacgatcctc gcacctacac ctgcatcttc 540

aactatctga acaaccctgt cttcactgtt accatcgtct gcatccactt cgtcctccct 600

ctcctcatcg tgggtttctg ctacgtgagg atctggacca aagtgctggc ggcccgtgac 660

cctgcagggc agaatcctga caaccaactt gctgaggttc gcaataaact aaccatgttt 720

gtgatcttcc tcctctttgc agtgtgctgg tgccctatca acgtgctcac tgtcttggtg 780

gctgtcagtc cgaaggagat ggcaggcaag atccccaact ggctttatct tgcagcctac 840

ttcatagcct acttcaacag ctgcctcaac gctgtgatct acgggctcct caatgagaat 900

ttccgaagag aatactggac catcttccat gctatgcggc accctatcat attcttctct 960

ggcctcatca gtgatattcg tgagatgcag gaggcccgta ccctggcccg cgcccgtgcc 1020

catgctcgcg accaagctcg tgaacaagac cgtgcccatg cctgtcctgc tgtggaggaa 1080

accccgatga atgtccggaa tgttccatta cctggtgatg ctgcagctgg ccaccccgac 1140

cgtgcctctg gccaccctaa gccccattcc agatcctcct ctgcctatcg caaatctgcc 1200

tctacccacc acaagtctgt ctttagccac tccaaggctg cctctggtca cctcaagcct 1260

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cccatcaagc cagctaccag ccatgctgag cccaccactg ctgactatcc caagcctgcc 1560

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<400> 142

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Lys Leu Pro Gln Pro Glu Tyr Pro Pro Ala Leu Ile Ile Phe Met Phe
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Cys Ala Met Val Ile Thr Ile Val Val Asp Leu Ile Gly Asn Ser Met
35 40 45

Val Ile Leu Ala Val Thr Lys Asn Lys Lys Leu Arg Asn Ser Gly Asn
50 55 60

Ile Phe Val Val Ser Leu Ser Val Ala Asp Met Leu Val Ala Ile Tyr

65 70 75 80

Pro Tyr Pro Leu Met Leu His Ala Met Ser Ile Gly Gly Trp Asp Leu
85 90 95

Ser Gln Leu Gln Cys Gln Met Val Gly Phe Ile Thr Gly Leu Ser Val
100 105 110

Val Gly Ser Ile Phe Asn Ile Val Ala Ile Ala Ile Asn Arg Tyr Cys
115 120 125

Tyr Ile Cys His Ser Leu Gln Tyr Glu Arg Ile Phe Ser Val Arg Asn
130 135 140

Thr Cys Ile Tyr Leu Val Ile Thr Trp Ile Met Thr Val Leu Ala Val
145 150 155 160

Leu Pro Asn Met Tyr Ile Gly Thr Ile Glu Tyr Asp Pro Arg Thr Tyr
165 170 175

Thr Cys Ile Phe Asn Tyr Leu Asn Asn Pro Val Phe Thr Val Thr Ile
180 185 190

Val Cys Ile His Phe Val Leu Pro Leu Leu Ile Val Gly Phe Cys Tyr
195 200 205

Val Arg Ile Trp Thr Lys Val Leu Ala Ala Arg Asp Pro Ala Gly Gln
210 215 220

Asn Pro Asp Asn Gln Leu Ala Glu Val Arg Asn Lys Leu Thr Met Phe
225 230 235 240

Val Ile Phe Leu Leu Phe Ala Val Cys Trp Cys Pro Ile Asn Val Leu
245 250 255

Thr Val Leu Val Ala Val Ser Pro Lys Glu Met Ala Gly Lys Ile Pro
260 265 270

Asn Trp Leu Tyr Leu Ala Ala Tyr Phe Ile Ala Tyr Phe Asn Ser Cys
275 280 285

Leu Asn Ala Val Ile Tyr Gly Leu Leu Asn Glu Asn Phe Arg Arg Glu
290 295 300

Tyr Trp Thr Ile Phe His Ala Met Arg His Pro Ile Ile Phe Phe Ser
305 310 315 320

Gly Leu Ile Ser Asp Ile Arg Glu Met Gln Glu Ala Arg Thr Leu Ala
325 330 335

Arg Ala Arg Ala His Ala Arg Asp Gln Ala Arg Glu Gln Asp Arg Ala
340 345 350

His Ala Cys Pro Ala Val Glu Glu Thr Pro Met Asn Val Arg Asn Val
355 360 365

Pro Leu Pro Gly Asp Ala Ala Ala Gly His Pro Asp Arg Ala Ser Gly
370 375 380

His Pro Lys Pro His Ser Arg Ser Ser Ser Ala Tyr Arg Lys Ser Ala
385 390 395 400

Ser Thr His His Lys Ser Val Phe Ser His Ser Lys Ala Ala Ser Gly
405 410 415

His Leu Lys Pro Val Ser Gly His Ser Lys Pro Ala Ser Gly His Pro
420 425 430

Lys Ser Ala Thr Val Tyr Pro Lys Pro Ala Ser Val His Phe Lys Ala
435 440 445

Asp Ser Val His Phe Lys Gly Asp Ser Val His Phe Lys Pro Asp Ser
450 455 460

Val His Phe Lys Pro Ala Ser Ser Asn Pro Lys Pro Ile Thr Gly His
465 470 475 480

His Val Ser Ala Gly Ser His Ser Lys Ser Ala Phe Asn Ala Ala Thr
485 490 495

Ser His Pro Lys Pro Ile Lys Pro Ala Thr Ser His Ala Glu Pro Thr
500 505 510

Thr Ala Asp Tyr Pro Lys Pro Ala Thr Thr Ser His Pro Lys Pro Ala
515 520 525

Ala Ala Asp Asn Pro Glu Leu Ser Ala Ser His Cys Pro Glu Ile Pro
530 535 540

Ala Ile Ala His Pro Val Ser Asp Asp Ser Asp Leu Pro Glu Ser Ala
545 550 555 560

Ser Ser Pro Ala Ala Gly Pro Thr Lys Pro Ala Ala Ser Gln Leu Glu
565 570 575

Ser Asp Thr Ile Ala Asp Leu Pro Asp Pro Thr Val Val Thr Thr Ser
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Thr Asn Asp Tyr His Asp Val Val Val Val Asp Val Glu Asp Asp Pro
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Asp Glu Met Ala Val
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<210> 145
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<210> 146
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<210> 147
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gatctggagt accccattga cgtcaatggg g 31

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